SEQUENCE LISTING

<110> Hofvander, Per
       Andersson, Mariette

<120> ENHANCED AMYLOSE PRODUCTION IN PLANTS

<130> 12810-00125-US

<150> PCT/EP2004/002096
<151> 2004-03-03

<150> EP03005181.7
<151> 2003-03-07

<160> 38

<170> PatentIn version 3.3

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gcg tat gcg act atg atg tat atg gga act ccg aga gac tac gag ttc   445
Ala Tyr Ala Thr Met Met Tyr Met Gly Thr Pro Arg Asp Tyr Glu Phe
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Tyr Val Ala Thr Arg Val Met Leu Arg Ser Leu Thr Arg Leu Gly Val
     50   55   60

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Glu Ala Asp Leu Val Val Ile Ala Ser Leu Asp Val Pro Leu Arg Trp

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Val Gln Thr Leu Glu Gln Glu Asp Gly Ala Lys Val Val Arg Val Lys
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aat ctg aac aat ccg tat tgt atc aac cct aat tgg aga ttc aag ctc    637
Asn Leu Asn Asn Pro Tyr Cys Ile Asn Pro Asn Trp Arg Phe Lys Leu
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aca ctg aac aaa ctt tat gcg tgg agc ctc gta aat tat gac agg gtt    685
Thr Leu Asn Lys Leu Tyr Ala Trp Ser Leu Val Asn Tyr Asp Arg Val
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gtc atg ctt gat gct gac aac ctt ttc ctc cag aaa act gat gaa ctg    733
Val Met Leu Asp Ala Asp Asn Leu Phe Leu Gln Lys Thr Asp Glu Leu
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Phe Gln Cys Gly Gln Phe Cys Ala Val Phe Ile Asn Pro Cys Ile Phe
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cac act ggt ctc ttt gta ttg cag cca tca aaa aag gtg ttc aat gac    829
His Thr Gly Leu Phe Val Leu Gln Pro Ser Lys Lys Val Phe Asn Asp
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atg atc cat gag ata gag att ggg agg gaa aat caa gac ggt gca gac    877
Met Ile His Glu Ile Glu Ile Gly Arg Glu Asn Gln Asp Gly Ala Asp
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caa ggt ttt att gga ggc cac ttc cca gat tta ctt gat cgg cca atg    925
Gln Gly Phe Ile Gly Gly His Phe Pro Asp Leu Leu Asp Arg Pro Met
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ttc cac cct cct ctt aat ggt acc cag ctc cag gga agt tac agg ctt    973
Phe His Pro Pro Leu Asn Gly Thr Gln Leu Gln Gly Ser Tyr Arg Leu
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cct cta gga tac caa atg gac gcc tct tat tat tat ctc aaa ctc cat    1021
Pro Leu Gly Tyr Gln Met Asp Ala Ser Tyr Tyr Tyr Leu Lys Leu His
225                     230                     235                     240

tgg tcg gta cct tgt gga cct aat agt gtc att aca ttt cct ggt gct    1069
Trp Ser Val Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly Ala
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cca tgg tta aaa cca tgg tat tgg tgg tca tgg cct gtc tta ccc ttg    1117
Pro Trp Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro Leu
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ggc atc cag tgg cat gaa cag cga cgt cta act gtt ggg tat ggt gct    1165
Gly Ile Gln Trp His Glu Gln Arg Arg Leu Thr Val Gly Tyr Gly Ala
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gag atg ata gca gtg ttg atc caa tct ata ttt tac cta gga ata att    1213
Glu Met Ile Ala Val Leu Ile Gln Ser Ile Phe Tyr Leu Gly Ile Ile
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cat gat gat agc aag agt gcc ttc tta cta cga act ggc ctt aaa ttg    1309
His Asp Asp Ser Lys Ser Ala Phe Leu Leu Arg Thr Gly Leu Lys Leu
            325         330             335

att gct ata tgg tcc att ctt gct gcc tac aca gtt cct tat ttc gtg    1357
Ile Ala Ile Trp Ser Ile Leu Ala Ala Tyr Thr Val Pro Tyr Phe Val
            340         345             350

att cct tgt aca gtt cat cca cta gtt ggc tgg agt ctc tac tta ctc    1405
Ile Pro Cys Thr Val His Pro Leu Val Gly Trp Ser Leu Tyr Leu Leu
            355         360             365

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Gly Ser Phe Ser Leu Ser Cys Ile Thr Val Asn Ala Phe Leu Leu Pro
370             375             380

atg cta cct gtt tta gtc cca tgg att ggg atc ctt ggg gcc ctt ttg    1501
Met Leu Pro Val Leu Val Pro Trp Ile Gly Ile Leu Gly Ala Leu Leu
385             390             395             400

gtg atg gct tac cct tgg tac aac gac ggt gtt gta aga gca atg gct    1549
Val Met Ala Tyr Pro Trp Tyr Asn Asp Gly Val Val Arg Ala Met Ala
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gta ttt aca tac gcc ttc tgt gct tct cca gca tta tgg atg gca ttg    1597
Val Phe Thr Tyr Ala Phe Cys Ala Ser Pro Ala Leu Trp Met Ala Leu
            420             425             430

gtt aaa atc aag tgt tct ctt cat gtt tca ctt gag agg gaa gga ttc    1645
Val Lys Ile Lys Cys Ser Leu His Val Ser Leu Glu Arg Glu Gly Phe
            435             440             445

ttg ccc aag ata agt gaa tct aca gca cct gct ggt tct aac aaa ctg    1693
Leu Pro Lys Ile Ser Glu Ser Thr Ala Pro Ala Gly Ser Asn Lys Leu
    450             455             460

tat tgaaagttga aaagttaaag gaatcaacag gagaactaat gcttcagaaa          1746
Tyr
465

catctccaaa cgttttgctt aggagacttg gagtctgctt gtgctatcct agctagttgc 1806

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            35                  40                  45

Tyr Val Ala Thr Arg Val Met Leu Arg Ser Leu Thr Arg Leu Gly Val
    50                  55                  60

Glu Ala Asp Leu Val Val Ile Ala Ser Leu Asp Val Pro Leu Arg Trp
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Val Gln Thr Leu Glu Gln Glu Asp Gly Ala Lys Val Val Arg Val Lys
                85                  90                  95

Asn Leu Asn Asn Pro Tyr Cys Ile Asn Pro Asn Trp Arg Phe Lys Leu
                100                 105                 110

Thr Leu Asn Lys Leu Tyr Ala Trp Ser Leu Val Asn Tyr Asp Arg Val
            115                 120                 125

Val Met Leu Asp Ala Asp Asn Leu Phe Leu Gln Lys Thr Asp Glu Leu
    130                 135                 140

Phe Gln Cys Gly Gln Phe Cys Ala Val Phe Ile Asn Pro Cys Ile Phe
145                 150                 155                 160

His Thr Gly Leu Phe Val Leu Gln Pro Ser Lys Lys Val Phe Asn Asp
                165                 170                 175

Met Ile His Glu Ile Glu Ile Gly Arg Glu Asn Gln Asp Gly Ala Asp
            180                 185                 190

Gln Gly Phe Ile Gly Gly His Phe Pro Asp Leu Leu Asp Arg Pro Met
            195                 200                 205

Phe His Pro Pro Leu Asn Gly Thr Gln Leu Gln Gly Ser Tyr Arg Leu
    210                 215                 220

Pro Leu Gly Tyr Gln Met Asp Ala Ser Tyr Tyr Tyr Leu Lys Leu His
225                 230                 235                 240

Trp Ser Val Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly Ala
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Pro Trp Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro Leu
                260                 265                 270
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Gly Ile Gln Trp His Glu Gln Arg Arg Leu Thr Val Gly Tyr Gly Ala
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Glu Met Ile Ala Val Leu Ile Gln Ser Ile Phe Tyr Leu Gly Ile Ile
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Ala Val Thr Arg Leu Ala Arg Pro Asn Leu Ser Lys Leu Cys Tyr Arg
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His Asp Asp Ser Lys Ser Ala Phe Leu Leu Arg Thr Gly Leu Lys Leu
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Ile Ala Ile Trp Ser Ile Leu Ala Ala Tyr Thr Val Pro Tyr Phe Val
                340   345   350

Ile Pro Cys Thr Val His Pro Leu Val Gly Trp Ser Leu Tyr Leu Leu
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Gly Ser Phe Ser Leu Ser Cys Ile Thr Val Asn Ala Phe Leu Leu Pro
        370   375   380

Met Leu Pro Val Leu Val Pro Trp Ile Gly Ile Leu Gly Ala Leu Leu
385   390   395   400

Val Met Ala Tyr Pro Trp Tyr Asn Asp Gly Val Val Arg Ala Met Ala
                405   410   415

Val Phe Thr Tyr Ala Phe Cys Ala Ser Pro Ala Leu Trp Met Ala Leu
                420   425   430

Val Lys Ile Lys Cys Ser Leu His Val Ser Leu Glu Arg Glu Gly Phe
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Leu Pro Lys Ile Ser Glu Ser Thr Ala Pro Ala Gly Ser Asn Lys Leu
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465

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acttgaaaaa ggaaagccca ga atg aga gga agt tta gct ggt gga cca cct 172

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agt cct att gaa cct aga cag agg ctt tct gta ttc act gag gaa aca   220
Ser Pro Ile Glu Pro Arg Gln Arg Leu Ser Val Phe Thr Glu Glu Thr
            15                  20                  25

agc aaa aga agg ttc ttg aga agt aaa gtt ttc aga gat ggg gag aga   268
Ser Lys Arg Arg Phe Leu Arg Ser Lys Val Phe Arg Asp Gly Glu Arg
            30                  35                  40

gct ctt cat agt ccc acc aaa aac agg aat ttt acc tgc aag ttc cca   316
Ala Leu His Ser Pro Thr Lys Asn Arg Asn Phe Thr Cys Lys Phe Pro
            45                  50                  55

act gtg aag ctt ata ttg ggt gtt att gct ctg gtt gca att tgg tca   364
Thr Val Lys Leu Ile Leu Gly Val Ile Ala Leu Val Ala Ile Trp Ser
        60                  65                  70

ctc tgg cat tct cca gca att tat aac acg gaa tac ata tct agt tca   412
Leu Trp His Ser Pro Ala Ile Tyr Asn Thr Glu Tyr Ile Ser Ser Ser
75                  80                  85                  90

ggc tct cgg gct gct ttg atg cac aga gag tta agt ggt cat tct tca   460
Gly Ser Arg Ala Ala Leu Met His Arg Glu Leu Ser Gly His Ser Ser
                95                  100                 105

gct gat caa cgt tat aca tca ctt tta gat att gac tgg gac caa att   508
Ala Asp Gln Arg Tyr Thr Ser Leu Leu Asp Ile Asp Trp Asp Gln Ile
            110                 115                 120

tcc caa gtt att gag aaa ctg gcc gat agg cat gag tat cag ggc gta   556
Ser Gln Val Ile Glu Lys Leu Ala Asp Arg His Glu Tyr Gln Gly Val
            125                 130                 135

ggg ata tta aac ttc aat gac agt gaa att gat cag ttg aag gag tta   604
Gly Ile Leu Asn Phe Asn Asp Ser Glu Ile Asp Gln Leu Lys Glu Leu
        140                 145                 150

cta ccg gac gct gag cat gta atc ttg aac ctg gat cac gtc ccg aat   652
Leu Pro Asp Ala Glu His Val Ile Leu Asn Leu Asp His Val Pro Asn
155                 160                 165                 170

aat ata aca tgg gaa aca ata tat cct gaa tgg ata gat gaa gaa gaa   700
Asn Ile Thr Trp Glu Thr Ile Tyr Pro Glu Trp Ile Asp Glu Glu Glu
                175                 180                 185

gaa ttt gag gtc ccc act tgt cct tct ctg ccc aaa att cag ttt ccg   748
Glu Phe Glu Val Pro Thr Cys Pro Ser Leu Pro Lys Ile Gln Phe Pro
            190                 195                 200

ggt aaa cca agg att gat ctc ata gtt gta aag ctt cca tgc aag aag   796
Gly Lys Pro Arg Ile Asp Leu Ile Val Val Lys Leu Pro Cys Lys Lys
            205                 210                 215

tct aag gac tgg tat aga gat gta gct cgt ttt cac ttg cag ctg gca   844
Ser Lys Asp Trp Tyr Arg Asp Val Ala Arg Phe His Leu Gln Leu Ala
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                  220                        225                      230
gca gca agg ctg gct gcc agt aat aaa ggg tat cat cca ata cat gtg      892
Ala Ala Arg Leu Ala Ala Ser Asn Lys Gly Tyr His Pro Ile His Val
235                     240                 245                 250

ctt ctg gtt act gag cat ttc cca acc ccc aat ctg ttc acc tgt aaa      940
Leu Leu Val Thr Glu His Phe Pro Thr Pro Asn Leu Phe Thr Cys Lys
                    255                 260                 265

gag tta gtt gta cgt gaa ggc aat gca tgg cta tat gaa cct aat ctg      988
Glu Leu Val Val Arg Glu Gly Asn Ala Trp Leu Tyr Glu Pro Asn Leu
                270                 275                 280

aac act tta aga gag aag ctc cac ctc cct gtt ggg tca tgt gaa ctt     1036
Asn Thr Leu Arg Glu Lys Leu His Leu Pro Val Gly Ser Cys Glu Leu
            285                 290                 295

gca gtt cct ctc aag gct aaa gca aat tgg cac tct gga aat gta aga     1084
Ala Val Pro Leu Lys Ala Lys Ala Asn Trp His Ser Gly Asn Val Arg
            300                 305                 310

cga gaa gcc tat gca act att ctc cac tca gca aat ttt tat gta tgt     1132
Arg Glu Ala Tyr Ala Thr Ile Leu His Ser Ala Asn Phe Tyr Val Cys
315                 320                 325                 330

gga gcc ata gct gca gca cag agt att cgc ttg gca ggt tca acc cga     1180
Gly Ala Ile Ala Ala Ala Gln Ser Ile Arg Leu Ala Gly Ser Thr Arg
                335                 340                 345

gat ctt gtg ata ctt gtt gat gag act atc agt gac tac cac agg ggt     1228
Asp Leu Val Ile Leu Val Asp Glu Thr Ile Ser Asp Tyr His Arg Gly
                350                 355                 360

ggt tta gag gct gcc gga tgg aag atc cac acg ata aag aga ata agg     1276
Gly Leu Glu Ala Ala Gly Trp Lys Ile His Thr Ile Lys Arg Ile Arg
                365                 370                 375

aat cct aaa gct gaa cag gat gcc tac aat gag tgg aac tat agc aaa     1324
Asn Pro Lys Ala Glu Gln Asp Ala Tyr Asn Glu Trp Asn Tyr Ser Lys
            380                 385                 390

ttt cgt ctc tgg cag ctg aca gat tat gac aaa atc atc ttc att gat     1372
Phe Arg Leu Trp Gln Leu Thr Asp Tyr Asp Lys Ile Ile Phe Ile Asp
395                 400                 405                 410

gcg gat ttg ttg ata ctg aga aat att gat ttt ctc ttt gag atg cct     1420
Ala Asp Leu Leu Ile Leu Arg Asn Ile Asp Phe Leu Phe Glu Met Pro
                415                 420                 425

gaa ata act gca ata gga aat aat gca acc ctt ttt aat tca ggc gtg     1468
Glu Ile Thr Ala Ile Gly Asn Asn Ala Thr Leu Phe Asn Ser Gly Val
                430                 435                 440

atg gtc gtt gaa cca tca aat tgc aca ttt cag ctg ttg atg gat cat     1516
Met Val Val Glu Pro Ser Asn Cys Thr Phe Gln Leu Leu Met Asp His
            445                 450                 455
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atc aat gag att gaa tca tac aat ggt ggg gat cag ggg tat ttg aac   1564
Ile Asn Glu Ile Glu Ser Tyr Asn Gly Gly Asp Gln Gly Tyr Leu Asn
    460             465             470

gaa ata ttc acc tgg tgg cat agg atc cca aaa cac atg aac ttt ttg   1612
Glu Ile Phe Thr Trp Trp His Arg Ile Pro Lys His Met Asn Phe Leu
475             480             485             490

aaa cat tat tgg gaa ggt gat gag gag gag aag aag caa atg aaa aca   1660
Lys His Tyr Trp Glu Gly Asp Glu Glu Glu Lys Lys Gln Met Lys Thr
            495             500             505

cgt ctt ttt ggt gct gat cct cca gtt ctc tat gtt ctg cac tac tta   1708
Arg Leu Phe Gly Ala Asp Pro Pro Val Leu Tyr Val Leu His Tyr Leu
            510             515             520

ggc ctg aaa cct tgg tta tgc ttc agg gac tac gat tgc aac tgg aat   1756
Gly Leu Lys Pro Trp Leu Cys Phe Arg Asp Tyr Asp Cys Asn Trp Asn
        525             530             535

gtg ggt aag ttg cag gag ttt gca agt gat gtg gca cac agg acg tgg   1804
Val Gly Lys Leu Gln Glu Phe Ala Ser Asp Val Ala His Arg Thr Trp
    540             545             550

tgg aag gtc cat gat gcc atg cca gat aac tta cat aaa tat tgt ttg   1852
Trp Lys Val His Asp Ala Met Pro Asp Asn Leu His Lys Tyr Cys Leu
555             560             565             570

ctt agg tct aaa cag aag gct gca cta gag tgg gat cga aga gaa gct   1900
Leu Arg Ser Lys Gln Lys Ala Ala Leu Glu Trp Asp Arg Arg Glu Ala
            575             580             585

gag aaa gct aac ttt tca gat ggt cat tgg aag atc aaa ata aag gac   1948
Glu Lys Ala Asn Phe Ser Asp Gly His Trp Lys Ile Lys Ile Lys Asp
            590             595             600

cca cgt ttg gag act tgt tat gaa gaa ttt tgc ttc tgg gaa agc atg   1996
Pro Arg Leu Glu Thr Cys Tyr Glu Glu Phe Cys Phe Trp Glu Ser Met
            605             610             615

tta tgg cac tgg ggt gaa aca aac tgg aca gat aat gcc acc tct tca   2044
Leu Trp His Trp Gly Glu Thr Asn Trp Thr Asp Asn Ala Thr Ser Ser
        620             625             630

cca aca cct ccc atg gtc aat act gct tca ctt tct tct ttg           2086
Pro Thr Pro Pro Met Val Asn Thr Ala Ser Leu Ser Ser Leu
635             640             645

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gaatgtcaac cagtgccatt agtatacatg gtgtcaacac tttccccacc cttgaaaaaa 2206

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Arg Ser Lys Val Phe Arg Asp Gly Glu Arg Ala Leu His Ser Pro Thr
            35                  40                  45

Lys Asn Arg Asn Phe Thr Cys Lys Phe Pro Thr Val Lys Leu Ile Leu
        50                  55                  60

Gly Val Ile Ala Leu Val Ala Ile Trp Ser Leu Trp His Ser Pro Ala
65                  70                  75                  80

Ile Tyr Asn Thr Glu Tyr Ile Ser Ser Ser Gly Ser Arg Ala Ala Leu
                85                  90                  95

Met His Arg Glu Leu Ser Gly His Ser Ser Ala Asp Gln Arg Tyr Thr
                100                 105                 110

Ser Leu Leu Asp Ile Asp Trp Asp Gln Ile Ser Gln Val Ile Glu Lys
            115                 120                 125

Leu Ala Asp Arg His Glu Tyr Gln Gly Val Gly Ile Leu Asn Phe Asn
        130                 135                 140

Asp Ser Glu Ile Asp Gln Leu Lys Glu Leu Leu Pro Asp Ala Glu His
145                 150                 155                 160

Val Ile Leu Asn Leu Asp His Val Pro Asn Asn Ile Thr Trp Glu Thr
                165                 170                 175

Ile Tyr Pro Glu Trp Ile Asp Glu Glu Glu Phe Glu Val Pro Thr
                180                 185                 190

Cys Pro Ser Leu Pro Lys Ile Gln Phe Pro Gly Lys Pro Arg Ile Asp
            195                 200                 205

Leu Ile Val Val Lys Leu Pro Cys Lys Lys Ser Lys Asp Trp Tyr Arg
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Asp Val Ala Arg Phe His Leu Gln Leu Ala Ala Ala Arg Leu Ala Ala
225                 230                 235                 240

Ser Asn Lys Gly Tyr His Pro Ile His Val Leu Leu Val Thr Glu His
            245                 250                 255

Phe Pro Thr Pro Asn Leu Phe Thr Cys Lys Glu Leu Val Val Arg Glu
            260                 265                 270

Gly Asn Ala Trp Leu Tyr Glu Pro Asn Leu Asn Thr Leu Arg Glu Lys
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Leu His Leu Pro Val Gly Ser Cys Glu Leu Ala Val Pro Leu Lys Ala
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Lys Ala Asn Trp His Ser Gly Asn Val Arg Arg Glu Ala Tyr Ala Thr
305             310             315             320

Ile Leu His Ser Ala Asn Phe Tyr Val Cys Gly Ala Ile Ala Ala Ala
                325             330             335

Gln Ser Ile Arg Leu Ala Gly Ser Thr Arg Asp Leu Val Ile Leu Val
            340             345             350

Asp Glu Thr Ile Ser Asp Tyr His Arg Gly Gly Leu Glu Ala Ala Gly
        355             360             365

Trp Lys Ile His Thr Ile Lys Arg Ile Arg Asn Pro Lys Ala Glu Gln
    370             375             380

Asp Ala Tyr Asn Glu Trp Asn Tyr Ser Lys Phe Arg Leu Trp Gln Leu
385             390             395             400

Thr Asp Tyr Asp Lys Ile Ile Phe Ile Asp Ala Asp Leu Leu Ile Leu
            405             410             415

Arg Asn Ile Asp Phe Leu Phe Glu Met Pro Glu Ile Thr Ala Ile Gly
            420             425             430

Asn Asn Ala Thr Leu Phe Asn Ser Gly Val Met Val Val Glu Pro Ser
            435             440             445

Asn Cys Thr Phe Gln Leu Leu Met Asp His Ile Asn Glu Ile Glu Ser
    450             455             460

Tyr Asn Gly Gly Asp Gln Gly Tyr Leu Asn Glu Ile Phe Thr Trp Trp
465             470             475             480

His Arg Ile Pro Lys His Met Asn Phe Leu Lys His Tyr Trp Glu Gly
            485             490             495

Asp Glu Glu Glu Lys Lys Gln Met Lys Thr Arg Leu Phe Gly Ala Asp
            500             505             510

Pro Pro Val Leu Tyr Val Leu His Tyr Leu Gly Leu Lys Pro Trp Leu
            515             520             525

Cys Phe Arg Asp Tyr Asp Cys Asn Trp Asn Val Gly Lys Leu Gln Glu
    530             535             540

Phe Ala Ser Asp Val Ala His Arg Thr Trp Trp Lys Val His Asp Ala
545             550             555             560

Met Pro Asp Asn Leu His Lys Tyr Cys Leu Leu Arg Ser Lys Gln Lys
            565             570             575

Ala Ala Leu Glu Trp Asp Arg Arg Glu Ala Glu Lys Ala Asn Phe Ser
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                580                    585                    590
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Asp Gly His Trp Lys Ile Lys Ile Lys Asp Pro Arg Leu Glu Thr Cys
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Tyr Glu Glu Phe Cys Phe Trp Glu Ser Met Leu Trp His Trp Gly Glu
    610   615   620

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Asn Thr Ala Ser Leu Ser Ser Leu
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 1   5   10   15

ttg atc atc aaa acg aca gcg tat aac gag aaa cag ctg ttc cag ccg   96
Leu Ile Ile Lys Thr Thr Ala Tyr Asn Glu Lys Gln Leu Phe Gln Pro
                20   25   30

ctt gaa acg gaa aac gca aac gcg atg acc gcg gtt atg gag cga gga   144
Leu Glu Thr Glu Asn Ala Asn Ala Met Thr Ala Val Met Glu Arg Gly
        35   40   45

tta aag acg cag cgg cgg ccg gag cac aag aac gct tat gcg acg atg   192
Leu Lys Thr Gln Arg Arg Pro Glu His Lys Asn Ala Tyr Ala Thr Met
    50   55   60

atg tac atg gga aca cca aga gac tac gag ttc tac gtt gcg aca cgt   240
Met Tyr Met Gly Thr Pro Arg Asp Tyr Glu Phe Tyr Val Ala Thr Arg
65   70   75   80

gtc ttg atc aga tcg ctt aag agt ctc cac gtg gac gct gat atc gtc   288
Val Leu Ile Arg Ser Leu Lys Ser Leu His Val Asp Ala Asp Ile Val
                85   90   95

gtt ata gcc tcc ctc gac gtt cct atc aac tgg att cac gct ctg gaa   336
Val Ile Ala Ser Leu Asp Val Pro Ile Asn Trp Ile His Ala Leu Glu
            100   105   110

gaa gaa gat gga gct aaa gta gtg aga gta gag aat ctt gag aat cca   384
Glu Glu Asp Gly Ala Lys Val Val Arg Val Glu Asn Leu Glu Asn Pro
        115   120   125
```

```
tac aag aaa caa acc aac ttc gac aac aga ttc aag ctt agt cta aac    432
Tyr Lys Lys Gln Thr Asn Phe Asp Asn Arg Phe Lys Leu Ser Leu Asn
    130             135             140

aag ctc tac gct tgg tct ctc tct gat tat gac cgt gtt gta atg ctt    480
Lys Leu Tyr Ala Trp Ser Leu Ser Asp Tyr Asp Arg Val Val Met Leu
145             150             155             160

gat gtc gac aat ctc ttt ctc aag aac acc gac gag ctc ttc cag tgt    528
Asp Val Asp Asn Leu Phe Leu Lys Asn Thr Asp Glu Leu Phe Gln Cys
            165             170             175

ggc caa ttt tgt gct gtc ttc atc aac cct tgc atc ttc cac act ggt    576
Gly Gln Phe Cys Ala Val Phe Ile Asn Pro Cys Ile Phe His Thr Gly
        180             185             190

ctc ttt gtg ttg cag cca tca atg gag gtc ttt aga gac atg ctt cat    624
Leu Phe Val Leu Gln Pro Ser Met Glu Val Phe Arg Asp Met Leu His
        195             200             205

gag ctt gaa gta aag aga gat aac cct gat gga gct gat caa ggc ttt    672
Glu Leu Glu Val Lys Arg Asp Asn Pro Asp Gly Ala Asp Gln Gly Phe
    210             215             220

ctt gtc agc tac ttc tct gat tta ctc aat cag cct ctc ttt cgt cct    720
Leu Val Ser Tyr Phe Ser Asp Leu Leu Asn Gln Pro Leu Phe Arg Pro
225             230             235             240

cct ccc gat aac cgc acc gcg ctt aag gga cat ttt agg ctt cct ttg    768
Pro Pro Asp Asn Arg Thr Ala Leu Lys Gly His Phe Arg Leu Pro Leu
            245             250             255

gga tat caa atg gac gca tct tat tac tac ctt aag ctc aga tgg aac    816
Gly Tyr Gln Met Asp Ala Ser Tyr Tyr Tyr Leu Lys Leu Arg Trp Asn
            260             265             270

gta cca tgt gga cca aac agt gtg ata acg ttc cca gga gca gta tgg    864
Val Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly Ala Val Trp
        275             280             285

tta aag cca tgg tat tgg tgg tca tgg cct gtt ctt cct tta ggc ctt    912
Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro Leu Gly Leu
        290             295             300

tca tgg cac cac caa cgc cgc tac acg att agt tat tca gca gag atg    960
Ser Trp His His Gln Arg Arg Tyr Thr Ile Ser Tyr Ser Ala Glu Met
305             310             315             320

cct tgg gtc cta acc caa gca gtg ttc tac cta gga att ata cta gtc    1008
Pro Trp Val Leu Thr Gln Ala Val Phe Tyr Leu Gly Ile Ile Leu Val
            325             330             335

aca cgt cta gcg cgt ccc aac atg acc aag cta tgt tac cga cgt tct    1056
Thr Arg Leu Ala Arg Pro Asn Met Thr Lys Leu Cys Tyr Arg Arg Ser
            340             345             350
```

```
gat aag aat cta agc atg atc cag aca gct ttc aag ttt gtt gca ctc      1104
Asp Lys Asn Leu Ser Met Ile Gln Thr Ala Phe Lys Phe Val Ala Leu
        355                 360             365

ctc ttt atc ctc tca gcc tac att ata cca ttc ttc atc atc cca cag      1152
Leu Phe Ile Leu Ser Ala Tyr Ile Ile Pro Phe Phe Ile Ile Pro Gln
        370             375                 380

acg atc cac ccg ctc att ggt tgg tct ctc tac tta acc ggc tcc ttt      1200
Thr Ile His Pro Leu Ile Gly Trp Ser Leu Tyr Leu Thr Gly Ser Phe
385                 390             395                 400

gct ctc tct acc ata ccc atc aac gcc ttc ttg ctt ccc att ctc cct      1248
Ala Leu Ser Thr Ile Pro Ile Asn Ala Phe Leu Leu Pro Ile Leu Pro
                405             410             415

gtc ata aca ccg tgg ctt ggc att ttc ggg aca ctc ctc gtg atg gct      1296
Val Ile Thr Pro Trp Leu Gly Ile Phe Gly Thr Leu Leu Val Met Ala
            420             425             430

ttt cct tct tat cct gat ggc gtt gtt aga gca ttg tcg gtt ttc ggg      1344
Phe Pro Ser Tyr Pro Asp Gly Val Val Arg Ala Leu Ser Val Phe Gly
        435             440             445

tat gca ttt tgt tgt gca ccg ttt cta tgg gtc tcc ttt gtg aag atc      1392
Tyr Ala Phe Cys Cys Ala Pro Phe Leu Trp Val Ser Phe Val Lys Ile
    450             455             460

aca tcg cat ctt cag att atg att gac aaa gag gtt ttg ttt ccg cgg      1440
Thr Ser His Leu Gln Ile Met Ile Asp Lys Glu Val Leu Phe Pro Arg
465                 470             475                 480

ttg ggt gaa tcc gga gtc act tct ggt ctc agc aaa ttg tac tga        1485
Leu Gly Glu Ser Gly Val Thr Ser Gly Leu Ser Lys Leu Tyr
                485                 490
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<210> 6
<211> 494
<212> PRT
<213> Arabidopsis thaliana

<400> 6
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Met Asp Leu Gln Arg Thr Leu Met Phe Ser Cys Trp Val Leu Ser Leu
1               5               10                  15
Leu Ile Ile Lys Thr Thr Ala Tyr Asn Glu Lys Gln Leu Phe Gln Pro
            20              25              30
Leu Glu Thr Glu Asn Ala Asn Ala Met Thr Ala Val Met Glu Arg Gly
        35              40              45
Leu Lys Thr Gln Arg Arg Pro Glu His Lys Asn Ala Tyr Ala Thr Met
    50              55              60
Met Tyr Met Gly Thr Pro Arg Asp Tyr Glu Phe Tyr Val Ala Thr Arg
65              70              75                  80
Val Leu Ile Arg Ser Leu Lys Ser Leu His Val Asp Ala Asp Ile Val
            85              90                  95
Val Ile Ala Ser Leu Asp Val Pro Ile Asn Trp Ile His Ala Leu Glu
            100             105             110
```

```
Glu Glu Asp Gly Ala Lys Val Val Arg Val Glu Asn Leu Glu Asn Pro
    115                 120             125
Tyr Lys Lys Gln Thr Asn Phe Asp Asn Arg Phe Lys Leu Ser Leu Asn
    130             135             140
Lys Leu Tyr Ala Trp Ser Leu Ser Asp Tyr Asp Arg Val Val Met Leu
145             150             155                 160
Asp Val Asp Asn Leu Phe Leu Lys Asn Thr Asp Glu Leu Phe Gln Cys
            165             170             175
Gly Gln Phe Cys Ala Val Phe Ile Asn Pro Cys Ile Phe His Thr Gly
            180             185             190
Leu Phe Val Leu Gln Pro Ser Met Glu Val Phe Arg Asp Met Leu His
    195             200             205
Glu Leu Glu Val Lys Arg Asp Asn Pro Asp Gly Ala Asp Gln Gly Phe
    210             215             220
Leu Val Ser Tyr Phe Ser Asp Leu Leu Asn Gln Pro Leu Phe Arg Pro
225             230             235             240
Pro Pro Asp Asn Arg Thr Ala Leu Lys Gly His Phe Arg Leu Pro Leu
            245             250             255
Gly Tyr Gln Met Asp Ala Ser Tyr Tyr Tyr Leu Lys Leu Arg Trp Asn
            260             265             270
Val Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly Ala Val Trp
            275             280             285
Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro Leu Gly Leu
    290             295             300
Ser Trp His His Gln Arg Arg Tyr Thr Ile Ser Tyr Ser Ala Glu Met
305             310             315             320
Pro Trp Val Leu Thr Gln Ala Val Phe Tyr Leu Gly Ile Ile Leu Val
            325             330             335
Thr Arg Leu Ala Arg Pro Asn Met Thr Lys Leu Cys Tyr Arg Arg Ser
            340             345             350
Asp Lys Asn Leu Ser Met Ile Gln Thr Ala Phe Lys Phe Val Ala Leu
            355             360             365
Leu Phe Ile Leu Ser Ala Tyr Ile Ile Pro Phe Phe Ile Ile Pro Gln
    370             375             380
Thr Ile His Pro Leu Ile Gly Trp Ser Leu Tyr Leu Thr Gly Ser Phe
385             390             395             400
Ala Leu Ser Thr Ile Pro Ile Asn Ala Phe Leu Leu Pro Ile Leu Pro
            405             410             415
Val Ile Thr Pro Trp Leu Gly Ile Phe Gly Thr Leu Leu Val Met Ala
            420             425             430
Phe Pro Ser Tyr Pro Asp Gly Val Val Arg Ala Leu Ser Val Phe Gly
            435             440             445
Tyr Ala Phe Cys Cys Ala Pro Phe Leu Trp Val Ser Phe Val Lys Ile
    450             455             460
Thr Ser His Leu Gln Ile Met Ile Asp Lys Glu Val Leu Phe Pro Arg
465             470             475             480
Leu Gly Glu Ser Gly Val Thr Ser Gly Leu Ser Lys Leu Tyr
            485             490
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<210> 7
<211> 1494
<212> DNA
<213> Arabidopsis thaliana

<220>

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<221> CDS
<222> (1)..(1494)

<400> 7
atg gat ttg cag aga ggc ttt gtg ttc ttg tct ttg gtt cta tct ttt      48
Met Asp Leu Gln Arg Gly Phe Val Phe Leu Ser Leu Val Leu Ser Phe
1               5                   10                  15

atg ata atc gaa acg acg gcg tat cga gag aga cag ctg ctg ctg ctg      96
Met Ile Ile Glu Thr Thr Ala Tyr Arg Glu Arg Gln Leu Leu Leu Leu
                20                  25                  30

caa cca ccg caa gaa acg gcg ata gat acc gca aac gcg gtg gtg acg     144
Gln Pro Pro Gln Glu Thr Ala Ile Asp Thr Ala Asn Ala Val Val Thr
            35                  40                  45

gtt caa gat cga ggt ttg aag acg cgg cga ccg gag cat aag aac gca     192
Val Gln Asp Arg Gly Leu Lys Thr Arg Arg Pro Glu His Lys Asn Ala
        50                  55                  60

tac gca acg atg atg tac atg ggg acg cca aga gac tac gag ttc tac     240
Tyr Ala Thr Met Met Tyr Met Gly Thr Pro Arg Asp Tyr Glu Phe Tyr
65                  70                  75                  80

gtt gcg aca cgt gtt ttg atc aga tcg ttg aga agt ctt cac gtg gaa     288
Val Ala Thr Arg Val Leu Ile Arg Ser Leu Arg Ser Leu His Val Glu
                85                  90                  95

gct gat ctc gtc gtc atc gct tct ctc gac gtt cct ctc cga tgg gtt     336
Ala Asp Leu Val Val Ile Ala Ser Leu Asp Val Pro Leu Arg Trp Val
            100                 105                 110

caa acc ttg gaa gag gaa gat gga gct aaa gtg gtg aga gtt gaa aat     384
Gln Thr Leu Glu Glu Glu Asp Gly Ala Lys Val Val Arg Val Glu Asn
            115                 120                 125

gtg gat aat cca tac agg aga cag acc aac ttc aac agt aga ttc aag     432
Val Asp Asn Pro Tyr Arg Arg Gln Thr Asn Phe Asn Ser Arg Phe Lys
        130                 135                 140

ctt act cta aac aag ctc tac gct tgg gct ttg tct gat tac gac cgt     480
Leu Thr Leu Asn Lys Leu Tyr Ala Trp Ala Leu Ser Asp Tyr Asp Arg
145                 150                 155                 160

gtg gtc atg cta gat gcc gat aac ctc ttt ctt aag aaa gcc gac gag     528
Val Val Met Leu Asp Ala Asp Asn Leu Phe Leu Lys Lys Ala Asp Glu
                165                 170                 175

ttg ttc cag tgt ggg cgc ttc tgt gcg gtc ttc att aac cct tgt atc     576
Leu Phe Gln Cys Gly Arg Phe Cys Ala Val Phe Ile Asn Pro Cys Ile
                180                 185                 190

ttc cac act ggt ctc ttc gtg ttg cag cca tca gtg gaa gtg ttc aag     624
Phe His Thr Gly Leu Phe Val Leu Gln Pro Ser Val Glu Val Phe Lys
            195                 200                 205

gac atg ctc cat gag cta caa gtt gga aga aag aat cct gat gga gct     672
```

```
Asp Met Leu His Glu Leu Gln Val Gly Arg Lys Asn Pro Asp Gly Ala
    210             215             220
```

```
gat caa ggt ttt ctt gtc agt tac ttc tct gat ctt ctt gac caa cct   720
Asp Gln Gly Phe Leu Val Ser Tyr Phe Ser Asp Leu Leu Asp Gln Pro
225             230             235             240
```

```
ctc ttt agt cct ccg agt aac gga tct gta ctt aat ggt cac ttg aga   768
Leu Phe Ser Pro Pro Ser Asn Gly Ser Val Leu Asn Gly His Leu Arg
            245             250             255
```

```
ctt ccc tta ggc tac caa atg gac gct tct tat ttc tat ctt aag cta   816
Leu Pro Leu Gly Tyr Gln Met Asp Ala Ser Tyr Phe Tyr Leu Lys Leu
            260             265             270
```

```
aga tgg aac ata ccc tgt gga cca aac agt gtg att aca ttc ccg gga   864
Arg Trp Asn Ile Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly
            275             280             285
```

```
gct gtt tgg tta aag cca tgg tac tgg tgg tca tgg cct gtt ctt cca   912
Ala Val Trp Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro
    290             295             300
```

```
cta ggt ttc tca tgg cac gag cag cgt cgc gcc act ata ggg tac tca   960
Leu Gly Phe Ser Trp His Glu Gln Arg Arg Ala Thr Ile Gly Tyr Ser
305             310             315             320
```

```
gcc gaa atg cct ttg gtt ata atc caa gca atg ttt tac ctt gga atc   1008
Ala Glu Met Pro Leu Val Ile Ile Gln Ala Met Phe Tyr Leu Gly Ile
            325             330             335
```

```
ata gtg gtt aca cga cta gct cgt cct aac ata acc aag cta tgt tat   1056
Ile Val Val Thr Arg Leu Ala Arg Pro Asn Ile Thr Lys Leu Cys Tyr
            340             345             350
```

```
cgc cgc tct gac cgc aac tta aca acg atc caa gct ggt ttt aag ttg   1104
Arg Arg Ser Asp Arg Asn Leu Thr Thr Ile Gln Ala Gly Phe Lys Leu
            355             360             365
```

```
atc gcg ctt ctc tct gta gtt gca gcc tac atc ttc cca ttc ttc acc   1152
Ile Ala Leu Leu Ser Val Val Ala Ala Tyr Ile Phe Pro Phe Phe Thr
370             375             380
```

```
atc cct cac act atc cac cca ctc atc ggc tgg tcg ctc tac ttg atg   1200
Ile Pro His Thr Ile His Pro Leu Ile Gly Trp Ser Leu Tyr Leu Met
385             390             395             400
```

```
gct tct ttt gct ctc tct tcc att tca atc aac act ctc ctc ctc cca   1248
Ala Ser Phe Ala Leu Ser Ser Ile Ser Ile Asn Thr Leu Leu Leu Pro
            405             410             415
```

```
acg ctc cct gtt ctc act cca tgg cta gga att ctc ggc act ctc ctt   1296
Thr Leu Pro Val Leu Thr Pro Trp Leu Gly Ile Leu Gly Thr Leu Leu
            420             425             430
```

```
gtc atg gcc ttc cct tgg tac cct gat gga gtg gtc aga gcc ttg tca   1344
Val Met Ala Phe Pro Trp Tyr Pro Asp Gly Val Val Arg Ala Leu Ser
```

```
                435                       440                       445
   gtt ttc gca tac gca ttt tgt tgc gca ccc ttt gtg tgg gtt tca ttc    1392
   Val Phe Ala Tyr Ala Phe Cys Cys Ala Pro Phe Val Trp Val Ser Phe
           450                 455                 460

   cgc aaa atc aca tcg cac ctc cag gtt ttg att gag aaa gag gtg ttg    1440
   Arg Lys Ile Thr Ser His Leu Gln Val Leu Ile Glu Lys Glu Val Leu
   465                 470                 475                 480

   ttc ccg cga ttg gga gac tca ggg gtc act tca ggc ttc agc aaa ttg    1488
   Phe Pro Arg Leu Gly Asp Ser Gly Val Thr Ser Gly Phe Ser Lys Leu
                   485                 490                 495

   tat tag                                                            1494
   Tyr
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<210> 8
<211> 497
<212> PRT
<213> Arabidopsis thaliana

<400> 8
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Met Asp Leu Gln Arg Gly Phe Val Phe Leu Ser Leu Val Leu Ser Phe
 1               5                  10                  15
Met Ile Ile Glu Thr Thr Ala Tyr Arg Glu Arg Gln Leu Leu Leu Leu
            20                  25                  30
Gln Pro Pro Gln Glu Thr Ala Ile Asp Thr Ala Asn Ala Val Val Thr
        35                  40                  45
Val Gln Asp Arg Gly Leu Lys Thr Arg Arg Pro Glu His Lys Asn Ala
    50                  55                  60
Tyr Ala Thr Met Met Tyr Met Gly Thr Pro Arg Asp Tyr Glu Phe Tyr
65                  70                  75                  80
Val Ala Thr Arg Val Leu Ile Arg Ser Leu Arg Ser Leu His Val Glu
                85                  90                  95
Ala Asp Leu Val Val Ile Ala Ser Leu Asp Val Pro Leu Arg Trp Val
            100                 105                 110
Gln Thr Leu Glu Glu Glu Asp Gly Ala Lys Val Val Arg Val Glu Asn
        115                 120                 125
Val Asp Asn Pro Tyr Arg Arg Gln Thr Asn Phe Asn Ser Arg Phe Lys
    130                 135                 140
Leu Thr Leu Asn Lys Leu Tyr Ala Trp Ala Leu Ser Asp Tyr Asp Arg
145                 150                 155                 160
Val Val Met Leu Asp Ala Asp Asn Leu Phe Leu Lys Lys Ala Asp Glu
                165                 170                 175
Leu Phe Gln Cys Gly Arg Phe Cys Ala Val Phe Ile Asn Pro Cys Ile
            180                 185                 190
Phe His Thr Gly Leu Phe Val Leu Gln Pro Ser Val Glu Val Phe Lys
        195                 200                 205
Asp Met Leu His Glu Leu Gln Val Gly Arg Lys Asn Pro Asp Gly Ala
    210                 215                 220
Asp Gln Gly Phe Leu Val Ser Tyr Phe Ser Asp Leu Leu Asp Gln Pro
225                 230                 235                 240
Leu Phe Ser Pro Pro Ser Asn Gly Ser Val Leu Asn Gly His Leu Arg
                245                 250                 255
Leu Pro Leu Gly Tyr Gln Met Asp Ala Ser Tyr Phe Tyr Leu Lys Leu
```

```
              260                      265                      270
Arg Trp Asn Ile Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly
         275                      280                      285
Ala Val Trp Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro
      290                      295                      300
Leu Gly Phe Ser Trp His Glu Gln Arg Arg Ala Thr Ile Gly Tyr Ser
305                      310                      315                      320
Ala Glu Met Pro Leu Val Ile Ile Gln Ala Met Phe Tyr Leu Gly Ile
                  325                      330                      335
Ile Val Val Thr Arg Leu Ala Arg Pro Asn Ile Thr Lys Leu Cys Tyr
               340                      345                      350
Arg Arg Ser Asp Arg Asn Leu Thr Thr Ile Gln Ala Gly Phe Lys Leu
            355                      360                      365
Ile Ala Leu Leu Ser Val Val Ala Ala Tyr Ile Phe Pro Phe Phe Thr
      370                      375                      380
Ile Pro His Thr Ile His Pro Leu Ile Gly Trp Ser Leu Tyr Leu Met
385                      390                      395                      400
Ala Ser Phe Ala Leu Ser Ser Ile Ser Ile Asn Thr Leu Leu Leu Pro
                  405                      410                      415
Thr Leu Pro Val Leu Thr Pro Trp Leu Gly Ile Leu Gly Thr Leu Leu
               420                      425                      430
Val Met Ala Phe Pro Trp Tyr Pro Asp Gly Val Val Arg Ala Leu Ser
            435                      440                      445
Val Phe Ala Tyr Ala Phe Cys Cys Ala Pro Phe Val Trp Val Ser Phe
      450                      455                      460
Arg Lys Ile Thr Ser His Leu Gln Val Leu Ile Glu Lys Glu Val Leu
465                      470                      475                      480
Phe Pro Arg Leu Gly Asp Ser Gly Val Thr Ser Gly Phe Ser Lys Leu
                  485                      490                      495
Tyr
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<210> 9
<211> 1944
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(1944)

<400> 9
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atg cat cca gct tca tgt agt ctc tca ctc agg aaa gtc aaa ctt aat    48
Met His Pro Ala Ser Cys Ser Leu Ser Leu Arg Lys Val Lys Leu Asn
 1               5                  10                  15

att ctt aca gtg aga atg aag ctc tct tct gaa agt ccc atg gcg ccg    96
Ile Leu Thr Val Arg Met Lys Leu Ser Ser Glu Ser Pro Met Ala Pro
             20                  25                  30

tca agt cag tca agt cat cga ctt tac att tcc agt gag aaa aca aaa   144
Ser Ser Gln Ser Ser His Arg Leu Tyr Ile Ser Ser Glu Lys Thr Lys
         35                  40                  45

acg aag aga ttc caa aga aac gga tac act ctc gat gtt gaa atg tgt   192
Thr Lys Arg Phe Gln Arg Asn Gly Tyr Thr Leu Asp Val Glu Met Cys
```

```
                 50                    55                    60

gtc aac ttc tct agt ctg aaa ctt gtt ttg ttt ctt atg atg ctg gtt    240
Val Asn Phe Ser Ser Leu Lys Leu Val Leu Phe Leu Met Met Leu Val
 65                    70                    75                    80

gct atg ttc aca ctc tac tgt tct cca ccg ttg caa att cct gaa gat    288
Ala Met Phe Thr Leu Tyr Cys Ser Pro Pro Leu Gln Ile Pro Glu Asp
                    85                    90                    95

cca tca agt ttt gca aac aaa tgg ata cta gaa cct gct gta acc aca    336
Pro Ser Ser Phe Ala Asn Lys Trp Ile Leu Glu Pro Ala Val Thr Thr
                   100                   105                   110

gat cct cgc tat ata gct aca tct gag atc aac tgg aac agt atg tca    384
Asp Pro Arg Tyr Ile Ala Thr Ser Glu Ile Asn Trp Asn Ser Met Ser
                   115                   120                   125

ctt gtt gtt gag cat tac tta tct ggc aga agc gag tat caa gga att    432
Leu Val Val Glu His Tyr Leu Ser Gly Arg Ser Glu Tyr Gln Gly Ile
                   130                   135                   140

ggc ttt cta aat ctc aac gat aac gag att aat cga tgg cag gtg gtc    480
Gly Phe Leu Asn Leu Asn Asp Asn Glu Ile Asn Arg Trp Gln Val Val
145                   150                   155                   160

ata aaa tct cac tgt cag cat ata gct ttg cat cta gac cat gct gca    528
Ile Lys Ser His Cys Gln His Ile Ala Leu His Leu Asp His Ala Ala
                   165                   170                   175

agt aac ata act tgg aaa tct tta tac ccg gaa tgg att gac gag gaa    576
Ser Asn Ile Thr Trp Lys Ser Leu Tyr Pro Glu Trp Ile Asp Glu Glu
                   180                   185                   190

gaa aaa ttc aaa gtc ccc act tgt cct tct ctt cct tgg att caa gtt    624
Glu Lys Phe Lys Val Pro Thr Cys Pro Ser Leu Pro Trp Ile Gln Val
                   195                   200                   205

cct gac aag tct cga atc gat ctt atc att gcc aag ctc cca tgt aac    672
Pro Asp Lys Ser Arg Ile Asp Leu Ile Ile Ala Lys Leu Pro Cys Asn
                   210                   215                   220

aag tca gga aaa tgg tca aga gat gtg gct aga ttg cac tta caa ctt    720
Lys Ser Gly Lys Trp Ser Arg Asp Val Ala Arg Leu His Leu Gln Leu
225                   230                   235                   240

gca gca gct cga gtg gcg gca tct tct gaa ggg ctt cat gat gtt cat    768
Ala Ala Ala Arg Val Ala Ala Ser Ser Glu Gly Leu His Asp Val His
                   245                   250                   255

gtg att ttg gta tca gat tgc ttt cca ata ccg aat ctt ttt acg ggt    816
Val Ile Leu Val Ser Asp Cys Phe Pro Ile Pro Asn Leu Phe Thr Gly
                   260                   265                   270

caa gaa ctt gtt gcc cgt caa gga aac ata tgg ctg tat aag cct aaa    864
Gln Glu Leu Val Ala Arg Gln Gly Asn Ile Trp Leu Tyr Lys Pro Lys
                   275                   280                   285
```

```
ctt cac cag tta aga caa aag tta caa ctt cct gtt ggt tcc tgt gaa     912
Leu His Gln Leu Arg Gln Lys Leu Gln Leu Pro Val Gly Ser Cys Glu
    290                 295                 300

ctt tct gtt cct ctt caa gct aaa gat aat ttc tac tcg gca aat gcc     960
Leu Ser Val Pro Leu Gln Ala Lys Asp Asn Phe Tyr Ser Ala Asn Ala
305                 310                 315                 320

aag aaa gaa gcg tac gcg acg atc ttg cac tca gat gat gct ttt gtc    1008
Lys Lys Glu Ala Tyr Ala Thr Ile Leu His Ser Asp Asp Ala Phe Val
                325                 330                 335

tgt gga gcc att gca gta gca cag agc att cga atg tca ggc tct act    1056
Cys Gly Ala Ile Ala Val Ala Gln Ser Ile Arg Met Ser Gly Ser Thr
                340                 345                 350

cgc aat ttg gta ata cta gtc gat gat tcg atc agt gaa tac cat aga    1104
Arg Asn Leu Val Ile Leu Val Asp Asp Ser Ile Ser Glu Tyr His Arg
                355                 360                 365

agt ggc ttg gaa tca gct gga tgg aag att cac aca ttt caa aga atc    1152
Ser Gly Leu Glu Ser Ala Gly Trp Lys Ile His Thr Phe Gln Arg Ile
    370                 375                 380

aga aac ccg aaa gct gaa gca aat gca tat aac caa tgg aac tac agc    1200
Arg Asn Pro Lys Ala Glu Ala Asn Ala Tyr Asn Gln Trp Asn Tyr Ser
385                 390                 395                 400

aaa ttc cgt ctt tgg gaa ttg aca gaa tac aac aag atc atc ttc att    1248
Lys Phe Arg Leu Trp Glu Leu Thr Glu Tyr Asn Lys Ile Ile Phe Ile
                405                 410                 415

gat gca gac atg ctt atc ctc aga aac atg gat ttc ctc ttc gag tac    1296
Asp Ala Asp Met Leu Ile Leu Arg Asn Met Asp Phe Leu Phe Glu Tyr
                420                 425                 430

ccc gaa atc tcc aca act gga aac gac ggt acg ctc ttc aac tcc ggt    1344
Pro Glu Ile Ser Thr Thr Gly Asn Asp Gly Thr Leu Phe Asn Ser Gly
                435                 440                 445

cta atg gtg att gaa cca tca aat tca aca ttc cag tta cta atg gat    1392
Leu Met Val Ile Glu Pro Ser Asn Ser Thr Phe Gln Leu Leu Met Asp
    450                 455                 460

cac atc aac gat atc aat tcc tac aat gga gga gac caa ggt tac ctt    1440
His Ile Asn Asp Ile Asn Ser Tyr Asn Gly Gly Asp Gln Gly Tyr Leu
465                 470                 475                 480

aac gag ata ttc aca tgg tgg cat cgg att cca aaa cac atg aat ttc    1488
Asn Glu Ile Phe Thr Trp Trp His Arg Ile Pro Lys His Met Asn Phe
                485                 490                 495

ttg aag cat ttc tgg gaa gga gac aca cct aag cac agg aaa tct aag    1536
Leu Lys His Phe Trp Glu Gly Asp Thr Pro Lys His Arg Lys Ser Lys
                500                 505                 510
```

```
acg aga cta ttt gga gct gat cct ccg ata ctc tac gtt ctt cat tac      1584
Thr Arg Leu Phe Gly Ala Asp Pro Pro Ile Leu Tyr Val Leu His Tyr
        515                 520                 525

cta ggt tac aac aaa cca tgg gta tgc ttc aga gac tac gat tgc aat      1632
Leu Gly Tyr Asn Lys Pro Trp Val Cys Phe Arg Asp Tyr Asp Cys Asn
        530                 535                 540

tgg aat gtc gtt gga tac cat caa ttc gcg agc gat gaa gca cac aaa      1680
Trp Asn Val Val Gly Tyr His Gln Phe Ala Ser Asp Glu Ala His Lys
545                 550                 555                 560

act tgg tgg aga gtg cac gac gcg atg cct aag aaa ttg cag agg ttt      1728
Thr Trp Trp Arg Val His Asp Ala Met Pro Lys Lys Leu Gln Arg Phe
                565                 570                 575

tgt cta ctg agt tcg aaa caa aag gcg caa ctt gag tgg gat cgg aga      1776
Cys Leu Leu Ser Ser Lys Gln Lys Ala Gln Leu Glu Trp Asp Arg Arg
            580                 585                 590

caa gct gag aaa gcg aat tac aga gac gga cat tgg agg att aag atc      1824
Gln Ala Glu Lys Ala Asn Tyr Arg Asp Gly His Trp Arg Ile Lys Ile
            595                 600                 605

aaa gat aag aga ctt acg act tgt ttt gaa gat ttc tgt ttc tgg gag      1872
Lys Asp Lys Arg Leu Thr Thr Cys Phe Glu Asp Phe Cys Phe Trp Glu
        610                 615                 620

agt atg ctt tgg cat tgg ggt gag act cag acc aac tcc acc gtc gct      1920
Ser Met Leu Trp His Trp Gly Glu Thr Gln Thr Asn Ser Thr Val Ala
625                 630                 635                 640

gct gat tct tcc tcc acc gcg taa                                       1944
Ala Asp Ser Ser Ser Thr Ala
                645
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<210> 10
<211> 647
<212> PRT
<213> Arabidopsis thaliana

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1               5                   10                  15
Ile Leu Thr Val Arg Met Lys Leu Ser Ser Glu Ser Pro Met Ala Pro
                20                  25                  30
Ser Ser Gln Ser Ser His Arg Leu Tyr Ile Ser Ser Glu Lys Thr Lys
            35                  40                  45
Thr Lys Arg Phe Gln Arg Asn Gly Tyr Thr Leu Asp Val Glu Met Cys
        50                  55                  60
Val Asn Phe Ser Ser Leu Lys Leu Val Leu Phe Leu Met Met Leu Val
65                  70                  75                  80
Ala Met Phe Thr Leu Tyr Cys Ser Pro Pro Leu Gln Ile Pro Glu Asp
                85                  90                  95
Pro Ser Ser Phe Ala Asn Lys Trp Ile Leu Glu Pro Ala Val Thr Thr
            100                 105                 110
```

Asp Pro Arg Tyr Ile Ala Thr Ser Glu Ile Asn Trp Asn Ser Met Ser
    115   120   125

Leu Val Val Glu His Tyr Leu Ser Gly Arg Ser Glu Tyr Gln Gly Ile
    130   135   140

Gly Phe Leu Asn Leu Asn Asp Asn Glu Ile Asn Arg Trp Gln Val Val
145   150   155   160

Ile Lys Ser His Cys Gln His Ile Ala Leu His Leu Asp His Ala Ala
              165   170   175

Ser Asn Ile Thr Trp Lys Ser Leu Tyr Pro Glu Trp Ile Asp Glu Glu
         180   185   190

Glu Lys Phe Lys Val Pro Thr Cys Pro Ser Leu Pro Trp Ile Gln Val
         195   200   205

Pro Asp Lys Ser Arg Ile Asp Leu Ile Ile Ala Lys Leu Pro Cys Asn
    210   215   220

Lys Ser Gly Lys Trp Ser Arg Asp Val Ala Arg Leu His Leu Gln Leu
225   230   235   240

Ala Ala Ala Arg Val Ala Ala Ser Ser Glu Gly Leu His Asp Val His
         245   250   255

Val Ile Leu Val Ser Asp Cys Phe Pro Ile Pro Asn Leu Phe Thr Gly
         260   265   270

Gln Glu Leu Val Ala Arg Gln Gly Asn Ile Trp Leu Tyr Lys Pro Lys
         275   280   285

Leu His Gln Leu Arg Gln Lys Leu Gln Leu Pro Val Gly Ser Cys Glu
    290   295   300

Leu Ser Val Pro Leu Gln Ala Lys Asp Asn Phe Tyr Ser Ala Asn Ala
305   310   315   320

Lys Lys Glu Ala Tyr Ala Thr Ile Leu His Ser Asp Asp Ala Phe Val
         325   330   335

Cys Gly Ala Ile Ala Val Ala Gln Ser Ile Arg Met Ser Gly Ser Thr
         340   345   350

Arg Asn Leu Val Ile Leu Val Asp Asp Ser Ile Ser Glu Tyr His Arg
         355   360   365

Ser Gly Leu Glu Ser Ala Gly Trp Lys Ile His Thr Phe Gln Arg Ile
    370   375   380

Arg Asn Pro Lys Ala Glu Ala Asn Ala Tyr Asn Gln Trp Asn Tyr Ser
385   390   395   400

Lys Phe Arg Leu Trp Glu Leu Thr Glu Tyr Asn Lys Ile Ile Phe Ile
         405   410   415

Asp Ala Asp Met Leu Ile Leu Arg Asn Met Asp Phe Leu Phe Glu Tyr
         420   425   430

Pro Glu Ile Ser Thr Thr Gly Asn Asp Gly Thr Leu Phe Asn Ser Gly
         435   440   445

Leu Met Val Ile Glu Pro Ser Asn Ser Thr Phe Gln Leu Leu Met Asp
    450   455   460

His Ile Asn Asp Ile Asn Ser Tyr Asn Gly Gly Asp Gln Gly Tyr Leu
465   470   475   480

Asn Glu Ile Phe Thr Trp Trp His Arg Ile Pro Lys His Met Asn Phe
         485   490   495

Leu Lys His Phe Trp Glu Gly Asp Thr Pro Lys His Arg Lys Ser Lys
         500   505   510

Thr Arg Leu Phe Gly Ala Asp Pro Pro Ile Leu Tyr Val Leu His Tyr
         515   520   525

Leu Gly Tyr Asn Lys Pro Trp Val Cys Phe Arg Asp Tyr Asp Cys Asn
    530   535   540

Trp Asn Val Val Gly Tyr His Gln Phe Ala Ser Asp Glu Ala His Lys
545   550   555   560

Thr Trp Trp Arg Val His Asp Ala Met Pro Lys Lys Leu Gln Arg Phe

```
                        565                     570                     575
Cys Leu Leu Ser Ser Lys Gln Lys Ala Gln Leu Glu Trp Asp Arg Arg
                580                     585                     590
Gln Ala Glu Lys Ala Asn Tyr Arg Asp Gly His Trp Arg Ile Lys Ile
                595                     600                     605
Lys Asp Lys Arg Leu Thr Thr Cys Phe Glu Asp Phe Cys Phe Trp Glu
            610                     615                     620
Ser Met Leu Trp His Trp Gly Glu Thr Gln Thr Asn Ser Thr Val Ala
625                     630                     635                     640
Ala Asp Ser Ser Ser Thr Ala
                        645
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<210> 11
<211> 1857
<212> DNA
<213> Arabidopsis thaliana

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<221> CDS
<222> (1)..(1857)

<400> 11

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atg ata cct tcc tca agt ccc atg gag tca aga cat cga ctc tcg ttc    48
Met Ile Pro Ser Ser Ser Pro Met Glu Ser Arg His Arg Leu Ser Phe
  1               5                  10                  15

tca aaa gag aag aca agt agg agg aga ttt caa aga att gag aag ggt    96
Ser Lys Glu Lys Thr Ser Arg Arg Arg Phe Gln Arg Ile Glu Lys Gly
                20                  25                  30

gtc aag ttc aac act ctg aaa ctt gtg ttg att tgt ata atg ctt gga   144
Val Lys Phe Asn Thr Leu Lys Leu Val Leu Ile Cys Ile Met Leu Gly
            35                  40                  45

gct ttg ttc acg atc tac cgt ttt cgt tat cca ccg cta caa att cct   192
Ala Leu Phe Thr Ile Tyr Arg Phe Arg Tyr Pro Pro Leu Gln Ile Pro
        50                  55                  60

gaa att cca act agt ttt ggt ctt act act gat cct cgc tat gta gct   240
Glu Ile Pro Thr Ser Phe Gly Leu Thr Thr Asp Pro Arg Tyr Val Ala
 65                  70                  75                  80

aca gct gag atc aac tgg aac cat atg tca aat ctt gtt gag aag cac   288
Thr Ala Glu Ile Asn Trp Asn His Met Ser Asn Leu Val Glu Lys His
                    85                  90                  95

gta ttt ggt aga agc gag tat caa gga att ggt ctt ata aat ctt aac   336
Val Phe Gly Arg Ser Glu Tyr Gln Gly Ile Gly Leu Ile Asn Leu Asn
                100                 105                 110

gat aac gag att gat cga ttc aag gag gta acg aaa tct gac tgt gat   384
Asp Asn Glu Ile Asp Arg Phe Lys Glu Val Thr Lys Ser Asp Cys Asp
            115                 120                 125

cat gta gct ttg cat cta gat tat gct gca aag aac ata aca tgg gaa   432
His Val Ala Leu His Leu Asp Tyr Ala Ala Lys Asn Ile Thr Trp Glu
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His Val Ala Leu His Leu Asp Tyr Ala Ala Lys Asn Ile Thr Trp Glu
    130                 135                 140

tct tta tac ccg gaa tgg att gat gaa gtt gaa gaa ttc gaa gtc cct   480
Ser Leu Tyr Pro Glu Trp Ile Asp Glu Val Glu Glu Phe Glu Val Pro
145                 150                 155                 160

act tgt cct tct ctg cct ttg att caa att cct ggc aag cct cgg att   528
Thr Cys Pro Ser Leu Pro Leu Ile Gln Ile Pro Gly Lys Pro Arg Ile
                165                 170                 175

gat ctt gta att gcc aag ctt ccg tgt gat aaa tca gga aaa tgg tct   576
Asp Leu Val Ile Ala Lys Leu Pro Cys Asp Lys Ser Gly Lys Trp Ser
                180                 185                 190

aga gat gtg gct cgc ttg cat tta caa ctt gca gca gct cga gtg gcg   624
Arg Asp Val Ala Arg Leu His Leu Gln Leu Ala Ala Ala Arg Val Ala
            195                 200                 205

gct tct tct aaa gga ctt cat aat gtt cat gtg att ttg gta tct gat   672
Ala Ser Ser Lys Gly Leu His Asn Val His Val Ile Leu Val Ser Asp
        210                 215                 220

tgc ttt cca ata ccg aat ctt ttt acg ggt caa gaa ctt gtt gcc cgt   720
Cys Phe Pro Ile Pro Asn Leu Phe Thr Gly Gln Glu Leu Val Ala Arg
225                 230                 235                 240

caa gga aac ata tgg ctg tat aag cct aat ctt cac cag cta aga caa   768
Gln Gly Asn Ile Trp Leu Tyr Lys Pro Asn Leu His Gln Leu Arg Gln
                245                 250                 255

aag tta cag ctt cct gtt ggt tcc tgt gaa ctt tct gtt cct ctt caa   816
Lys Leu Gln Leu Pro Val Gly Ser Cys Glu Leu Ser Val Pro Leu Gln
                260                 265                 270

gct aaa gat aat ttc tac tcc gca ggt gca aag aaa gaa gct tac gcg   864
Ala Lys Asp Asn Phe Tyr Ser Ala Gly Ala Lys Lys Glu Ala Tyr Ala
                275                 280                 285

act atc ttg cat tct gcc caa ttt tat gtc tgt gga gcc att gca gct   912
Thr Ile Leu His Ser Ala Gln Phe Tyr Val Cys Gly Ala Ile Ala Ala
        290                 295                 300

gca cag agc att cga atg tca ggc tct act cgt gat ctg gtc ata ctt   960
Ala Gln Ser Ile Arg Met Ser Gly Ser Thr Arg Asp Leu Val Ile Leu
305                 310                 315                 320

gtt gat gaa acg ata agc gaa tac cat aaa agt ggc ttg gta gct gct  1008
Val Asp Glu Thr Ile Ser Glu Tyr His Lys Ser Gly Leu Val Ala Ala
                325                 330                 335

gga tgg aag att caa atg ttt caa aga atc agg aac ccg aat gct gta  1056
Gly Trp Lys Ile Gln Met Phe Gln Arg Ile Arg Asn Pro Asn Ala Val
                340                 345                 350

cca aat gcc tac aac gaa tgg aac tac agc aag ttt cgt ctt tgg caa  1104
Pro Asn Ala Tyr Asn Glu Trp Asn Tyr Ser Lys Phe Arg Leu Trp Gln
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         355                    360                    365

ctg act gaa tac agt aag atc atc ttc atc gat gca gac atg ctt atc    1152
Leu Thr Glu Tyr Ser Lys Ile Ile Phe Ile Asp Ala Asp Met Leu Ile
    370             375                 380

ctg aga aac att gat ttc ctc ttc gag ttc cct gag ata tca gca act    1200
Leu Arg Asn Ile Asp Phe Leu Phe Glu Phe Pro Glu Ile Ser Ala Thr
385                 390                 395                 400

gga aac aat gct acg ctc ttc aac tct ggt cta atg gtg gtt gag cca    1248
Gly Asn Asn Ala Thr Leu Phe Asn Ser Gly Leu Met Val Val Glu Pro
                405                 410                 415

tct aat tca aca ttc cag tta cta atg gat aac att aat gaa gtt gtg    1296
Ser Asn Ser Thr Phe Gln Leu Leu Met Asp Asn Ile Asn Glu Val Val
            420                 425                 430

tct tac aac gga gga gac caa ggt tac ctt aac gag ata ttc aca tgg    1344
Ser Tyr Asn Gly Gly Asp Gln Gly Tyr Leu Asn Glu Ile Phe Thr Trp
            435                 440                 445

tgg cat cgg att cca aaa cac atg aat ttc ttg aag cat ttc tgg gaa    1392
Trp His Arg Ile Pro Lys His Met Asn Phe Leu Lys His Phe Trp Glu
    450                 455                 460

gga gac gaa cct gag att aaa aaa atg aag acg agt cta ttt gga gct    1440
Gly Asp Glu Pro Glu Ile Lys Lys Met Lys Thr Ser Leu Phe Gly Ala
465                 470                 475                 480

gat cct ccg atc cta tac gtt ctt cat tac cta ggt tat aac aaa ccc    1488
Asp Pro Pro Ile Leu Tyr Val Leu His Tyr Leu Gly Tyr Asn Lys Pro
                485                 490                 495

tgg tta tgc ttc aga gac tat gac tgc aat tgg aat gtc gat att ttc    1536
Trp Leu Cys Phe Arg Asp Tyr Asp Cys Asn Trp Asn Val Asp Ile Phe
            500                 505                 510

cag gaa ttt gct agt gac gag gct cat aaa acc tgg tgg aga gtg cac    1584
Gln Glu Phe Ala Ser Asp Glu Ala His Lys Thr Trp Trp Arg Val His
            515                 520                 525

gac gca atg cct gaa aac ttg cat aag ttc tgt cta cta aga tcg aaa    1632
Asp Ala Met Pro Glu Asn Leu His Lys Phe Cys Leu Leu Arg Ser Lys
    530                 535                 540

cag aag gcg caa ctt gaa tgg gat agg aga caa gca gag aaa ggg aac    1680
Gln Lys Ala Gln Leu Glu Trp Asp Arg Arg Gln Ala Glu Lys Gly Asn
545                 550                 555                 560

tac aaa gat gga cat tgg aag ata aag atc aaa gac aag aga ctt aag    1728
Tyr Lys Asp Gly His Trp Lys Ile Lys Ile Lys Asp Lys Arg Leu Lys
                565                 570                 575

act tgt ttc gaa gat ttc tgc ttt tgg gag agt atg ctt tgg cat tgg    1776
Thr Cys Phe Glu Asp Phe Cys Phe Trp Glu Ser Met Leu Trp His Trp
            580                 585                 590
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ggt gag acg aac tct acc aac aat tct tcc acc acc acc act tca tca    1824
Gly Glu Thr Asn Ser Thr Asn Asn Ser Ser Thr Thr Thr Thr Ser Ser
        595             600             605

ccg ccg cat aaa acc gct ctc cct tcc ctg tga                        1857
Pro Pro His Lys Thr Ala Leu Pro Ser Leu
        610             615
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<212> PRT
<213> Arabidopsis thaliana

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Ser Lys Glu Lys Thr Ser Arg Arg Arg Phe Gln Arg Ile Glu Lys Gly
            20                  25                  30
Val Lys Phe Asn Thr Leu Lys Leu Val Leu Ile Cys Ile Met Leu Gly
            35                  40                  45
Ala Leu Phe Thr Ile Tyr Arg Phe Arg Tyr Pro Pro Leu Gln Ile Pro
    50                  55                  60
Glu Ile Pro Thr Ser Phe Gly Leu Thr Thr Asp Pro Arg Tyr Val Ala
 65                  70                  75                  80
Thr Ala Glu Ile Asn Trp Asn His Met Ser Asn Leu Val Glu Lys His
                85                  90                  95
Val Phe Gly Arg Ser Glu Tyr Gln Gly Ile Gly Leu Ile Asn Leu Asn
            100                 105                 110
Asp Asn Glu Ile Asp Arg Phe Lys Glu Val Thr Lys Ser Asp Cys Asp
            115                 120                 125
His Val Ala Leu His Leu Asp Tyr Ala Ala Lys Asn Ile Thr Trp Glu
    130                 135                 140
Ser Leu Tyr Pro Glu Trp Ile Asp Glu Val Glu Glu Phe Glu Val Pro
145                 150                 155                 160
Thr Cys Pro Ser Leu Pro Leu Ile Gln Ile Pro Gly Lys Pro Arg Ile
                165                 170                 175
Asp Leu Val Ile Ala Lys Leu Pro Cys Asp Lys Ser Gly Lys Trp Ser
                180                 185                 190
Arg Asp Val Ala Arg Leu His Leu Gln Leu Ala Ala Ala Arg Val Ala
            195                 200                 205
Ala Ser Ser Lys Gly Leu His Asn Val His Val Ile Leu Val Ser Asp
    210                 215                 220
Cys Phe Pro Ile Pro Asn Leu Phe Thr Gly Gln Glu Leu Val Ala Arg
225                 230                 235                 240
Gln Gly Asn Ile Trp Leu Tyr Lys Pro Asn Leu His Gln Leu Arg Gln
                245                 250                 255
Lys Leu Gln Leu Pro Val Gly Ser Cys Glu Leu Ser Val Pro Leu Gln
            260                 265                 270
Ala Lys Asp Asn Phe Tyr Ser Ala Gly Ala Lys Lys Glu Ala Tyr Ala
            275                 280                 285
Thr Ile Leu His Ser Ala Gln Phe Tyr Val Cys Gly Ala Ile Ala Ala
    290                 295                 300
Ala Gln Ser Ile Arg Met Ser Gly Ser Thr Arg Asp Leu Val Ile Leu
305                 310                 315                 320
Val Asp Glu Thr Ile Ser Glu Tyr His Lys Ser Gly Leu Val Ala Ala
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                      325                    330                    335
Gly Trp Lys Ile Gln Met Phe Gln Arg Ile Arg Asn Pro Asn Ala Val
                340                    345                    350
Pro Asn Ala Tyr Asn Glu Trp Asn Tyr Ser Lys Phe Arg Leu Trp Gln
            355                    360                    365
Leu Thr Glu Tyr Ser Lys Ile Ile Phe Ile Asp Ala Asp Met Leu Ile
        370                    375                    380
Leu Arg Asn Ile Asp Phe Leu Phe Glu Phe Pro Glu Ile Ser Ala Thr
385                    390                    395                    400
Gly Asn Asn Ala Thr Leu Phe Asn Ser Gly Leu Met Val Val Glu Pro
                405                    410                    415
Ser Asn Ser Thr Phe Gln Leu Leu Met Asp Asn Ile Asn Glu Val Val
                420                    425                    430
Ser Tyr Asn Gly Gly Asp Gln Gly Tyr Leu Asn Glu Ile Phe Thr Trp
            435                    440                    445
Trp His Arg Ile Pro Lys His Met Asn Phe Leu Lys His Phe Trp Glu
        450                    455                    460
Gly Asp Glu Pro Glu Ile Lys Lys Met Lys Thr Ser Leu Phe Gly Ala
465                    470                    475                    480
Asp Pro Pro Ile Leu Tyr Val Leu His Tyr Leu Gly Tyr Asn Lys Pro
                485                    490                    495
Trp Leu Cys Phe Arg Asp Tyr Asp Cys Asn Trp Asn Val Asp Ile Phe
                500                    505                    510
Gln Glu Phe Ala Ser Asp Glu Ala His Lys Thr Trp Trp Arg Val His
            515                    520                    525
Asp Ala Met Pro Glu Asn Leu His Lys Phe Cys Leu Leu Arg Ser Lys
        530                    535                    540
Gln Lys Ala Gln Leu Glu Trp Asp Arg Arg Gln Ala Glu Lys Gly Asn
545                    550                    555                    560
Tyr Lys Asp Gly His Trp Lys Ile Lys Ile Lys Asp Lys Arg Leu Lys
                565                    570                    575
Thr Cys Phe Glu Asp Phe Cys Phe Trp Glu Ser Met Leu Trp His Trp
                580                    585                    590
Gly Glu Thr Asn Ser Thr Asn Asn Ser Ser Thr Thr Thr Thr Ser Ser
                595                    600                    605
Pro Pro His Lys Thr Ala Leu Pro Ser Leu
610                    615
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<210> 13
<211> 2130
<212> DNA
<213> Arabidopsis thaliana

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<221> CDS
<222> (1)..(1980)

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atg gca aac tct ccc gct gct cct gca ccc acc acc aca acc ggt ggt    48
Met Ala Asn Ser Pro Ala Ala Pro Ala Pro Thr Thr Thr Thr Gly Gly
1               5                   10                  15

gac tcc cgg cga cgc ctc tcc gcg tcc ata gaa gca ata tgc aag agg    96
Asp Ser Arg Arg Arg Leu Ser Ala Ser Ile Glu Ala Ile Cys Lys Arg
            20                  25                  30
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aga ttc cgg aga aat agc aaa gga ggt ggc aga tcg gat atg gtg aaa    144
Arg Phe Arg Arg Asn Ser Lys Gly Gly Gly Arg Ser Asp Met Val Lys
        35                  40                  45

ccg ttt aat atc ata aat ttt tcg aca caa gac aaa aac agt agt tgt    192
Pro Phe Asn Ile Ile Asn Phe Ser Thr Gln Asp Lys Asn Ser Ser Cys
    50                  55                  60

tgt tgt ttc acc aag ttt cag atc gtg aag ctt ctc ttg ttt atc ctt    240
Cys Cys Phe Thr Lys Phe Gln Ile Val Lys Leu Leu Leu Phe Ile Leu
65                  70                  75                  80

ctc tct gcc act ctc ttc acc att atc tat tct cct gaa gct tat cat    288
Leu Ser Ala Thr Leu Phe Thr Ile Ile Tyr Ser Pro Glu Ala Tyr His
                85                  90                  95

cat tct ctt tcc cac tca tct tct cga tgg ata tgg aga aga caa gat    336
His Ser Leu Ser His Ser Ser Ser Arg Trp Ile Trp Arg Arg Gln Asp
            100             105                 110

cca cgt tac ttc tcg gat ctg gat ata aac tgg gac gat gtg act aaa    384
Pro Arg Tyr Phe Ser Asp Leu Asp Ile Asn Trp Asp Asp Val Thr Lys
        115                 120                 125

acc ctt gag aac atc gaa gaa ggc cgt acg atc ggt gtc ttg aat ttt    432
Thr Leu Glu Asn Ile Glu Glu Gly Arg Thr Ile Gly Val Leu Asn Phe
    130                 135                 140

gat tcg aac gag atc caa cga tgg aga gaa gta tcc aag agc aag gac    480
Asp Ser Asn Glu Ile Gln Arg Trp Arg Glu Val Ser Lys Ser Lys Asp
145                 150                 155                 160

aat ggg gat gaa gaa aaa gtt gtt gta ttg aat cta gat tac gca gac   ·528
Asn Gly Asp Glu Glu Lys Val Val Val Leu Asn Leu Asp Tyr Ala Asp
                165                 170                 175

aag aat gtg act tgg gac gca cta tat cca gag tgg atc gat gag gag    576
Lys Asn Val Thr Trp Asp Ala Leu Tyr Pro Glu Trp Ile Asp Glu Glu
            180                 185                 190

caa gaa aca gag gtc cct gtt tgt cct aat atc ccg aac att aag gta    624
Gln Glu Thr Glu Val Pro Val Cys Pro Asn Ile Pro Asn Ile Lys Val
        195                 200                 205

cct aca aga aga ctc gat ctg atc gtc gtg aaa ctt cct tgt cgg aaa    672
Pro Thr Arg Arg Leu Asp Leu Ile Val Val Lys Leu Pro Cys Arg Lys
    210                 215                 220

gaa ggg aat tgg tcg aga gac gtc ggg aga ttg cat cta cag cta gcg    720
Glu Gly Asn Trp Ser Arg Asp Val Gly Arg Leu His Leu Gln Leu Ala
225                 230                 235                 240

gct gca act gtg gcg gct tcg gcc aaa ggg ttt ttc agg gga cat gtg    768
Ala Ala Thr Val Ala Ala Ser Ala Lys Gly Phe Phe Arg Gly His Val
            245                 250                 255
```

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ttt ttt gta tct aga tgc ttt ccg att ccg aat ctt ttc cgg tgt aaa   816
Phe Phe Val Ser Arg Cys Phe Pro Ile Pro Asn Leu Phe Arg Cys Lys
            260             265             270

gat ctt gtg tct cgg aga ggc gat gtt tgg ttg tac aaa cct aat ctt   864
Asp Leu Val Ser Arg Arg Gly Asp Val Trp Leu Tyr Lys Pro Asn Leu
            275             280             285

gat acc ttg aga gac aag ctt cag ctg cct gta ggg tct tgt gag cta   912
Asp Thr Leu Arg Asp Lys Leu Gln Leu Pro Val Gly Ser Cys Glu Leu
        290             295             300

tct ctt cct ctt ggc atc caa gat agg cca agc tta gga aac cct aaa   960
Ser Leu Pro Leu Gly Ile Gln Asp Arg Pro Ser Leu Gly Asn Pro Lys
305             310             315             320

aga gaa gct tac gca aca att ctt cac tca gct cac gtt tac gtc tgc  1008
Arg Glu Ala Tyr Ala Thr Ile Leu His Ser Ala His Val Tyr Val Cys
                325             330             335

ggt gca atc gcc gcg gct cag agc ata aga cag tct ggt tcg acg aga  1056
Gly Ala Ile Ala Ala Ala Gln Ser Ile Arg Gln Ser Gly Ser Thr Arg
            340             345             350

gac ctt gtt atc ctt gtt gat gac aac atc agc ggt tac cac cgg agt  1104
Asp Leu Val Ile Leu Val Asp Asp Asn Ile Ser Gly Tyr His Arg Ser
            355             360             365

gga cta gaa gcc gcg ggt tgg caa atc cgg acg ata cag agg att cga  1152
Gly Leu Glu Ala Ala Gly Trp Gln Ile Arg Thr Ile Gln Arg Ile Arg
        370             375             380

aac cct aag gca gag aaa gat gct tac aac gaa tgg aac tac agc aag  1200
Asn Pro Lys Ala Glu Lys Asp Ala Tyr Asn Glu Trp Asn Tyr Ser Lys
385             390             395             400

ttc cgg cta tgg cag ctg act gat tac gac aaa atc att ttc atc gac  1248
Phe Arg Leu Trp Gln Leu Thr Asp Tyr Asp Lys Ile Ile Phe Ile Asp
                405             410             415

gcg gat ctc tta atc ttg aga aac atc gat ttc ttg ttc tcg atg cct  1296
Ala Asp Leu Leu Ile Leu Arg Asn Ile Asp Phe Leu Phe Ser Met Pro
            420             425             430

gag atc tca gct aca gga aac aat gga act ctg ttt aat tca gga gtt  1344
Glu Ile Ser Ala Thr Gly Asn Asn Gly Thr Leu Phe Asn Ser Gly Val
            435             440             445

atg gtg atc gag cct tgc aac tgt acg ttt cag ctt ctg atg gaa cat  1392
Met Val Ile Glu Pro Cys Asn Cys Thr Phe Gln Leu Leu Met Glu His
            450             455             460

ata aac gag att gag tct tat aac ggt gga gat caa ggt tac tta aac  1440
Ile Asn Glu Ile Glu Ser Tyr Asn Gly Gly Asp Gln Gly Tyr Leu Asn
465             470             475             480

gag gta ttc aca tgg tgg cac cgg att cca aaa cat atg aat ttc ttg  1488
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```
    Glu Val Phe Thr Trp Trp His Arg Ile Pro Lys His Met Asn Phe Leu
                    485             490             495


    aag cat ttt tgg att ggc gat gaa gat gac gcg aaa cgc aag aaa aca    1536
    Lys His Phe Trp Ile Gly Asp Glu Asp Asp Ala Lys Arg Lys Lys Thr
                    500             505             510


    gag ctt ttt gga gca gag cct cct gtt ctt tat gtt ctt cat tac ctt    1584
    Glu Leu Phe Gly Ala Glu Pro Pro Val Leu Tyr Val Leu His Tyr Leu
                515             520             525


    ggg atg aag ccg tgg tta tgt tac cgt gac tac gac tgt aac ttc aac    1632
    Gly Met Lys Pro Trp Leu Cys Tyr Arg Asp Tyr Asp Cys Asn Phe Asn
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    tcc gac ata ttc gtt gag ttt gct acc gat atc gct cat cga aaa tgg    1680
    Ser Asp Ile Phe Val Glu Phe Ala Thr Asp Ile Ala His Arg Lys Trp
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    tgg atg gtc cac gac gcc atg cca cag gaa ctt cac caa ttc tgt tac    1728
    Trp Met Val His Asp Ala Met Pro Gln Glu Leu His Gln Phe Cys Tyr
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    ttg cga tcc aag caa aag gca cag ctg gaa tat gat cgc cgg caa gca    1776
    Leu Arg Ser Lys Gln Lys Ala Gln Leu Glu Tyr Asp Arg Arg Gln Ala
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    gag gcc gca aat tat gcc gac ggt cat tgg aaa ata aga gta aag gac    1824
    Glu Ala Ala Asn Tyr Ala Asp Gly His Trp Lys Ile Arg Val Lys Asp
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    ccg aga ttc aaa att tgc atc gac aaa tta tgt aat tgg aaa agt atg    1872
    Pro Arg Phe Lys Ile Cys Ile Asp Lys Leu Cys Asn Trp Lys Ser Met
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    ctg cgg cat tgg ggc gaa tca aat tgg act gac tac gag tct ttt gtt    1920
    Leu Arg His Trp Gly Glu Ser Asn Trp Thr Asp Tyr Glu Ser Phe Val
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    ccc acc cca cca gcc att acc gta gac cgg aga tca tca ctt ccc ggc    1968
    Pro Thr Pro Pro Ala Ile Thr Val Asp Arg Arg Ser Ser Leu Pro Gly
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    His Asn Leu


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Met Ala Ala Ala Thr Thr Thr Thr Thr Thr Ser Ser Ser Ile Ser Phe
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tcc acc aaa cca tct cct tcc tcc tcc aaa tca cca tta cca atc tcc    96
Ser Thr Lys Pro Ser Pro Ser Ser Ser Lys Ser Pro Leu Pro Ile Ser
            20                  25                  30

aga ttc tcc ctc cca ttc tcc cta aac ccc aac aaa tca tcc tcc tcc   144
Arg Phe Ser Leu Pro Phe Ser Leu Asn Pro Asn Lys Ser Ser Ser Ser
        35                  40                  45

tcc cgc cgc cgc ggt atc aaa tcc agc tct ccc tcc tcc atc tcc gcc   192
Ser Arg Arg Arg Gly Ile Lys Ser Ser Ser Pro Ser Ser Ile Ser Ala
    50                  55                  60

gtg ctc aac aca acc acc aat gtc aca acc act ccc tct cca acc aaa   240
Val Leu Asn Thr Thr Thr Asn Val Thr Thr Thr Pro Ser Pro Thr Lys
 65                  70                  75                  80

cct acc aaa ccc gaa aca ttc atc tcc cga ttc gct cca gat caa ccc   288
Pro Thr Lys Pro Glu Thr Phe Ile Ser Arg Phe Ala Pro Asp Gln Pro
                85                  90                  95

cgc aaa ggc gct gat att ctc gtc gag gct tta gaa cgt caa ggc gta   336
Arg Lys Gly Ala Asp Ile Leu Val Glu Ala Leu Glu Arg Gln Gly Val
            100                 105                 110

gaa acc gta ttc gct tac cct gga ggt gca tca atg gag att cac caa   384
Glu Thr Val Phe Ala Tyr Pro Gly Gly Ala Ser Met Glu Ile His Gln
        115                 120                 125

gcc tta acc cgc tct tcc tca atc cgt aac gtc ctt cct cgt cac gaa   432
Ala Leu Thr Arg Ser Ser Ser Ile Arg Asn Val Leu Pro Arg His Glu
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caa gga ggt gta ttc gca gca gaa gga tac gct cga tcc tca ggt aaa    480
Gln Gly Gly Val Phe Ala Ala Glu Gly Tyr Ala Arg Ser Ser Gly Lys
145             150                 155                 160

cca ggt atc tgt ata gcc act tca ggt ccc gga gct aca aat ctc gtt    528
Pro Gly Ile Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
                165                 170                 175

agc gga tta gcc gat gcg ttg tta gat agt gtt cct ctt gta gca atc    576
Ser Gly Leu Ala Asp Ala Leu Leu Asp Ser Val Pro Leu Val Ala Ile
            180                 185                 190

aca gga caa gtc cct cgt cgt atg att ggt aca gat gcg ttt caa gag    624
Thr Gly Gln Val Pro Arg Arg Met Ile Gly Thr Asp Ala Phe Gln Glu
            195                 200                 205

act ccg att gtt gag gta acg cgt tcg att acg aag cat aac tat ctt    672
Thr Pro Ile Val Glu Val Thr Arg Ser Ile Thr Lys His Asn Tyr Leu
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gtg atg gat gtt gaa gat att cct agg att att gag gag gct ttc ttt    720
Val Met Asp Val Glu Asp Ile Pro Arg Ile Ile Glu Glu Ala Phe Phe
225                 230                 235                 240

tta gct act tct ggt aga cct gga cct gtt ttg gtt gat gtt cct aaa    768
Leu Ala Thr Ser Gly Arg Pro Gly Pro Val Leu Val Asp Val Pro Lys
                245                 250                 255

gat att caa caa cag ctt gcg att cct aat tgg gaa cag gct atg aga    816
Asp Ile Gln Gln Gln Leu Ala Ile Pro Asn Trp Glu Gln Ala Met Arg
            260                 265                 270

tta cct ggt tat atg tct agg atg cct aaa cct ccg gaa gat tct cat    864
Leu Pro Gly Tyr Met Ser Arg Met Pro Lys Pro Pro Glu Asp Ser His
            275                 280                 285

ttg gag cag att gtt agg ttg att tct gag tct aag aag cct gtg ttg    912
Leu Glu Gln Ile Val Arg Leu Ile Ser Glu Ser Lys Lys Pro Val Leu
    290                 295                 300

tat gtt ggt ggt ggt tgt ttg aac tct agc gat gaa ttg ggt agg ttt    960
Tyr Val Gly Gly Gly Cys Leu Asn Ser Ser Asp Glu Leu Gly Arg Phe
305                 310                 315                 320

gtt gag ctt acg gga atc cct gtt gcg agt acg ttg atg ggg ctg gga   1008
Val Glu Leu Thr Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu Gly
            325                 330                 335

tct tat cct tgt gat gat gag ttg tcg tta cat atg ctt gga atg cat   1056
Ser Tyr Pro Cys Asp Asp Glu Leu Ser Leu His Met Leu Gly Met His
            340                 345                 350

ggg act gtg tat gca aat tac gct gtg gag cat agt gat ttg ttg ttg   1104
Gly Thr Val Tyr Ala Asn Tyr Ala Val Glu His Ser Asp Leu Leu Leu
            355                 360                 365
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gcg ttt ggg gta agg ttt gat gat cgt gtc acg ggt aaa ctt gag gct    1152
Ala Phe Gly Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu Ala
        370             375             380

ttt gct agt agg gct aag att gtt cat att gat att gac tcg gct gag    1200
Phe Ala Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu
385             390             395             400

att ggg aag aat aag act cct cat gtg tct gtg tgt ggt gat gtt aag    1248
Ile Gly Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val Lys
            405             410             415

ctg gct ttg caa ggg atg aat aag gtt ctt gag aac cga gcg gag gag    1296
Leu Ala Leu Gln Gly Met Asn Lys Val Leu Glu Asn Arg Ala Glu Glu
            420             425             430

ctt aaa ctt gat ttt gga gtt tgg agg aat gag ttg aac gta cag aaa    1344
Leu Lys Leu Asp Phe Gly Val Trp Arg Asn Glu Leu Asn Val Gln Lys
            435             440             445

cag aag ttt ccg ttg agc ttt aag acg ttt ggg gaa gct att cct cca    1392
Gln Lys Phe Pro Leu Ser Phe Lys Thr Phe Gly Glu Ala Ile Pro Pro
        450             455             460

cag tat gcg att aag gtc ctt gat gag ttg act gat gga aaa gcc ata    1440
Gln Tyr Ala Ile Lys Val Leu Asp Glu Leu Thr Asp Gly Lys Ala Ile
465             470             475             480

ata agt act ggt gtc ggg caa cat caa atg tgg gcg gcg cag ttc tac    1488
Ile Ser Thr Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe Tyr
            485             490             495

aat tac aag aaa cca agg cag tgg cta tca tca gga ggc ctt gga gct    1536
Asn Tyr Lys Lys Pro Arg Gln Trp Leu Ser Ser Gly Gly Leu Gly Ala
            500             505             510

atg gga ttt gga ctt cct gct gcg att gga gcg tct gtt gct aac cct    1584
Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Ser Val Ala Asn Pro
            515             520             525

gat gcg ata gtt gtg gat att gac gga gat gga agt ttt ata atg aat    1632
Asp Ala Ile Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn
        530             535             540

gtg caa gag cta gcc act att cgt gta gag aat ctt cca gtg aag gta    1680
Val Gln Glu Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Val
545             550             555             560

ctt tta tta aac aac cag cat ctt ggc atg gtt atg caa tgg gaa gat    1728
Leu Leu Leu Asn Asn Gln His Leu Gly Met Val Met Gln Trp Glu Asp
            565             570             575

cgg ttc tac aaa gct aac cga gca cac aca ttt ctc gga gat ccg gct    1776
Arg Phe Tyr Lys Ala Asn Arg Ala His Thr Phe Leu Gly Asp Pro Ala
        580             585             590
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cag gag gac gag ata ttc ccg aac atg ttg ctg ttt gca gca gct tgc   1824
Gln Glu Asp Glu Ile Phe Pro Asn Met Leu Leu Phe Ala Ala Ala Cys
        595                 .600                605

ggg att cca gcg gcg agg gtg aca aag aaa gca gat ctc cga gaa gct   1872
Gly Ile Pro Ala Ala Arg Val Thr Lys Lys Ala Asp Leu Arg Glu Ala   .
        610                 615                 620

att cag aca atg ctg gat aca.cca gga cct tac ctg ttg gat gtg att   1920
Ile Gln Thr Met Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Val .Ile
625                 630                 635                 .640

tgt ccg cac caa gaa cat gtg ttg ccg atg atc ccg aat ggt ggc act   1968
Cys Pro His Gln Glu His Val Leu Pro Met Ile Pro Asn Gly Gly Thr   .
                645                 650                655

ttc aac gat gtc ata acg gaa gga gat ggc cgg att aaa tac tgagagctc 2019
Phe Asn Asp Val Ile Thr Glu Gly Asp Gly Arg Ile Lys Tyr
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Arg Phe Ser Leu Pro Phe Ser Leu Asn Pro Asn Lys Ser Ser Ser Ser
            35                  40                  45

Ser Arg Arg Arg Gly Ile Lys Ser Ser Ser Pro Ser Ser Ile Ser Ala
        50                  55                  60

Val Leu Asn Thr Thr Thr Asn Val Thr Thr Thr Pro Ser Pro Thr Lys
 65                  70                  75                  80

Pro Thr Lys Pro Glu Thr Phe Ile Ser Arg Phe Ala Pro Asp Gln Pro
                85                  90                  95

Arg Lys Gly Ala Asp Ile Leu Val Glu Ala Leu Glu Arg Gln Gly Val
            100                 105                 110

Glu Thr Val Phe Ala Tyr Pro Gly Gly Ala Ser Met Glu Ile His Gln
            115                 120                 125

Ala Leu Thr Arg Ser Ser Ser Ile Arg Asn Val Leu Pro Arg His Glu
        130                 135                 140

Gln Gly Gly Val Phe Ala Ala Glu Gly Tyr Ala Arg Ser Ser Gly Lys
145                 150                 155                 160
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Pro Gly Ile Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
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Ser Gly Leu Ala Asp Ala Leu Leu Asp Ser Val Pro Leu Val Ala Ile
            180                 185                 190

Thr Gly Gln Val Pro Arg Arg Met Ile Gly Thr Asp Ala Phe Gln Glu
        195                 200             205

Thr Pro Ile Val Glu Val Thr Arg Ser Ile Thr Lys His Asn Tyr Leu
    210                 215                 220

Val Met Asp Val Glu Asp Ile Pro Arg Ile Ile Glu Glu Ala Phe Phe
225                 230                 235                 240

Leu Ala Thr Ser Gly Arg Pro Gly Pro Val Leu Val Asp Val Pro Lys
            245                 250                 255

Asp Ile Gln Gln Gln Leu Ala Ile Pro Asn Trp Glu Gln Ala Met Arg
            260                 265                 270

Leu Pro Gly Tyr Met Ser Arg Met Pro Lys Pro Pro Glu Asp Ser His
        275                 280                 285

Leu Glu Gln Ile Val Arg Leu Ile Ser Glu Ser Lys Lys Pro Val Leu
    290                 295                 300

Tyr Val Gly Gly Gly Cys Leu Asn Ser Ser Asp Glu Leu Gly Arg Phe
305                 310                 315                 320

Val Glu Leu Thr Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu Gly
            325                 330                 335

Ser Tyr Pro Cys Asp Asp Glu Leu Ser Leu His Met Leu Gly Met His
            340                 345                 350

Gly Thr Val Tyr Ala Asn Tyr Ala Val Glu His Ser Asp Leu Leu Leu
            355                 360                 365

Ala Phe Gly Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu Ala
    370                 375                 380

Phe Ala Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu
385                 390                 395                 400

Ile Gly Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val Lys
            405                 410                 415

Leu Ala Leu Gln Gly Met Asn Lys Val Leu Glu Asn Arg Ala Glu Glu
            420                 425                 430

Leu Lys Leu Asp Phe Gly Val Trp Arg Asn Glu Leu Asn Val Gln Lys
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Gln Lys Phe Pro Leu Ser Phe Lys Thr Phe Gly Glu Ala Ile Pro Pro
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Gln Tyr Ala Ile Lys Val Leu Asp Glu Leu Thr Asp Gly Lys Ala Ile
465   470   475   480

Ile Ser Thr Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe Tyr
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Asn Tyr Lys Lys Pro Arg Gln Trp Leu Ser Ser Gly Gly Leu Gly Ala
            500   505   510

Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Ser Val Ala Asn Pro
        515   520   525

Asp Ala Ile Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn
    530   535   540

Val Gln Glu Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Val
545   550   555   560

Leu Leu Leu Asn Asn Gln His Leu Gly Met Val Met Gln Trp Glu Asp
            565   570   575

Arg Phe Tyr Lys Ala Asn Arg Ala His Thr Phe Leu Gly Asp Pro Ala
        580   585   590

Gln Glu Asp Glu Ile Phe Pro Asn Met Leu Leu Phe Ala Ala Ala Cys
        595   600   605

Gly Ile Pro Ala Ala Arg Val Thr Lys Lys Ala Asp Leu Arg Glu Ala
    610   615   620

Ile Gln Thr Met Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Val Ile
625   630   635   640

Cys Pro His Gln Glu His Val Leu Pro Met Ile Pro Asn Gly Gly Thr
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Phe Asn Asp Val Ile Thr Glu Gly Asp Gly Arg Ile Lys Tyr
            660   665   670

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tatattaatg ttttaaattc ctttatagtg ataaagatgg ttcgaaacat gctacaaatt 180
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tagataccag cccgggccg   259

<210> 19
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<212> DNA
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agtgagctac taccaacagc caatatcgag gagagtgacg   400

<210> 20
<211> 1105
<212> DNA
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<220>
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<223> Description of Artificial Sequence:RNAifragment

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ttaactgaag ttgcattgat gaaaaattat actatgtttt atgtatatat attaattttt 540
aaattccttt atagtgataa agatagttcg aaacatgcta taaattatta tacgaattta 600
cgttactttt tttaatctac tttaacaatt ttctaatttc actattgaac atagataccа 660
gcccgggccg tcgacctcga attcgccctt ggagagtgac gttcgcgtca ctctcctcga 720
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tgcgttcgtc aactctgtaa taagccacac atgttcgcgc aggagacagc actttgaagg 840
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aatggcaacc accatctcgc atttgagaga agatacctaa gtacctccca gtttccatag 960
ttaaagaggc gggaatccca catccaatga taaccacgag ctccagagtg aaagtaacaa 1020
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acgatgtcca tgagaacaac aattc   1105

<210> 21
<211> 180

<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)..(180)
<223> Description of Artificial Sequence:SBE RNAi 1

<400> 21
actagtggta cttaggtatc ttctctcaaa tgcgagatgg tggttgagtg agctactacc 60
aacagccaat atcgaggaga gtgacgttcg cgtcactctc ctcgatattg gctgttggta 120
gtagctcact caaccaccat ctcgcatttg agagaagata cctaagtacc ttttggtacc 180

<210> 22
<211> 420
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)..(420)
<223> Description of Artificial Sequence:SBE RNAi 2

<400> 22
actagttgga gctcgtggtt atcattggat gtgggattcc cgcctcttta actatggaaa 60
ctgggaggta cttaggtatc ttctctcaaa tgcgagatgg tggttggctt attacagagt 120
tgacgaacgc atgtcagaaa ctgaagttta ccagacagac atttctagtg agctactacc 180
aacagccaat atcgaggaga gtgacgttcg cgtcactctc ctcgatattg gctgttggta 240
gtagctcact agaaatgtct gtctggtaaa cttcagtttc tgacatgcgt tcgtcaactc 300
tgtaataagc caaccaccat ctcgcatttg agagaagata cctaagtacc tcccagtttc 360
catagttaaa gaggcgggaa tcccacatcc aatgataacc acgagctcca ttttggtacc 420

<210> 23
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)..(37)
<223> Description of Artificial Sequence:spacer

<400> 23
atcaagctta tcgataccgt cgacctcgaa gcttgat   37

<210> 24
<211> 837
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)..(837)
<223> Description of Artificial Sequence:fragment of be2

and be1 in pHAS3 for RNAi

<400> 24
gaattgttgt tctcatggac atcgttcaca gccatgcatc aaataatact ttagatggac 60
tgaacatgtt tgacggcacc gatagttgtt actttcactc tggagctcgt ggttatcatt 120
ggatgtggga ttcccgcctc tttaactatg gaaactggga ggtacttagg tatcttctct 180
caaatgcgag atggtggttg ccatttcaca tcaccagaag gaatacctgg agttccagaa 240
acaaatttca atggtcgtcc aaattccttc aaagtgctgt ctcctgcgcg aacatgtgtg 300
gcttattaca gagttgacga acgcatgtca gaaactgaag tttaccagac agacatttct 360
agtgagctac taccaacagc caatatcgag gagagtgacg atcaagctta tcgataccgt 420
cgacctcgaa gcttgatcgt cactctcctc gatattggct gttggtagta gctcactaga 480
aatgtctgtc tggtaaactt cagtttctga catgcgttcg tcaactctgt aataagccac 540
acatgttcgc gcaggagaca gcactttgaa ggaatttgga cgaccattga aatttgtttc 600
tggaactcca ggtattcctt ctggtgatgt gaaatggcaa ccaccatctc gcatttgaga 660
gaagatacct aagtacctcc cagtttccat agttaaagag gcgggaatcc cacatccaat 720
gataaccacg agctccagag tgaaagtaac aactatcggt gccgtcaaac atgttcagtc 780
catctaaagt attatttgat gcatggctgt gaacgatgtc catgagaaca acaattc 837

<210> 25
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(24)
<223> Npt2_for primer

<400> 25
agcaaggtga gatgacagga gatc   24

<210> 26
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(22)
<223> Npt2_rev primer

<400> 26
cagacaatcg gctgctctga tg   22

<210> 27
<211> 22
<212> DNA
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<220>
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<222> (1)..(22)
<223> AHAS1_frw primer

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<400>  27
aacaacaaca tcttcttcga tc                                        22


<210>  28
<211>  20
<212>  DNA
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<220>
<221> misc_feature
<222> (1)..(20)
<223>  AHAS1_rev primer

<400>  28
taacgagatt tgtagctccg                                           20


<210>  29
<211>  20
<212>  DNA
<213>  Artificial sequence

<220>
<221> misc_feature
<222> (1)..(20)
<223>  StGH1 sense RNA primer

<400>  29
tgaagacagc acaaaactgg                                           20


<210>  30
<211>  20
<212>  DNA
<213>  Artificial sequence

<220>
<221> misc_feature
<222> (1)..(20)
<223>  StGH1 antisense RNA primer

<400>  30
gtgaaagttt gaacgcacac                                           20


<210>  31
<211>  20
<212>  DNA
<213>  Artificial sequence

<220>
<221> misc_feature
<222> (1)..(20)
<223>  StGH2 sense RNA primer

<400>  31
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agtgccataa catgctttcc                                                    20


<210>  32
<211>  21
<212>  DNA
<213>  Artificial sequence

<220>
<221> misc_feature
<222> (1)..(21)
<223>  StGH2 antisense RNA primer

<400>  32
cacatttcag ctgttgatgg a                                                  21


<210>  33
<211>  21
<212>  DNA
<213>  Artificial sequence

<220>
<221> misc_feature
<222> (1)..(21)
<223>  StGH1 forward primer

<400>  33
tcgagtcgcc acgtagaact c                                                  21


<210>  34
<211>  23
<212>  DNA
<213>  Artificial sequence

<220>
<221> misc_feature
<222> (1)..(23)
<223>  StGH1 reverse primer

<400>  34
gaaatgcgta tgcgactatg atg                                                23


<210>  35
<211>  16
<212>  DNA
<213>  Artificial sequence

<220>
<221> misc_feature
<222> (1)..(16)
<223>  StGH1 TaqMan probe

<400>  35
agtctctcgg agttcc                                                        16
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<210>  36
<211>  22
<212>  DNA
<213>  Artificial sequence

<220>
<221> misc_feature
<222> (1)..(22)
<223>  StGH2 forward primer

<400>  36
ggtgctgatc ctccagttct ct                                        22


<210>  37
<211>  22
<212>  DNA
<213>  Artificial sequence

<220>
<221> misc_feature
<222> (1)..(22)
<223>  StGH2 reverse primer

<400>  37
gtccctgaag cataaccaag gt                                        22


<210>  38
<211>  19
<212>  DNA
<213>  Artificial sequence

<220>
<221> misc_feature
<222> (1)..(19)
<223>  StGH2 TaqMan probe

<400>  38
ttctgcacta cttaggcct                                            19
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